

# 49753

## SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: KAREN A. CANELLA Examiner #: 77681 Date: 8/28/01  
 Art Unit: 1642 Phone Number 308-4362 Serial Number: 691503, 089  
 Mail Box and Bldg/Room Location: 8D 03 Results Format Preferred (circle) PAPER DISK E-MAIL  
8E12

If more than one search is submitted, please prioritize searches in order of need.

\*\*\*\*\*

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers; and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: \_\_\_\_\_

Inventors (please provide full names): \_\_\_\_\_

Earliest Priority Filing Date: \_\_\_\_\_

\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

SEARCH AND INTERFERENCE SEARCH

IN THE PROTEIN DATABASES ONLY

- ① SEQ ID NO: 2
- ② SEQ ID NO: 4
- ③ SEQ ID NO: 5

*suffix Aug 28*

RECEIVED  
AUG 28 2001  
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FOR OFFICIAL USE ONLY

### STAFF USE ONLY

Type of Search

Vendors and cost where applicable

Searcher: Ch. Hines NA Sequence (#) \_\_\_\_\_ STN \_\_\_\_\_  
 Searcher Phone #: 308-4501 TAA Sequence (#) 3 Dialog \_\_\_\_\_  
 Searcher Location: Biology Lib. Structure (#) \_\_\_\_\_ Questel/Orbit \_\_\_\_\_  
 Date Searcher Picked Up: 8/28/01 Bibliographic \_\_\_\_\_ Dr. Link \_\_\_\_\_  
 Date Completed: 8/31/01 Litigation \_\_\_\_\_ Lexis/Nexis \_\_\_\_\_  
 Searcher Prep & Review Time: \_\_\_\_\_ Fulltext \_\_\_\_\_ Sequence Systems ABSS62  
 Clerical Prep Time: 5 min Patent Family \_\_\_\_\_ WWW/Internet \_\_\_\_\_  
 Online Time: 3 min Other \_\_\_\_\_ Other (specify) \_\_\_\_\_

**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 28, 2001, 17:11:14 ; Search time 242.67 Seconds  
(without alignments)  
360.192 Million cell updates/sec

Title: US-09-503-089a-5  
2042  
Sequence: 1 MKRONVRLALIVCTFTYLL.....STGLHSLSTFGMLMKRRSSV 394

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2803329 seqs, 221847457 residues  
Total number of hits satisfying chosen parameters: 2803329

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_AA\_Main:\*

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3: /cgn2\_6/ptodata/2/paa/US07\_COMB.pep:\*  
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22: /cgn2\_6/ptodata/2/paa/US098\_COMB.pep:\*  
23: /cgn2\_6/ptodata/2/paa/US099\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2042	100.0	394	15	US-09-144-914-4
2	2042	100.0	394	18	US-09-436-265-4
3	2042	100.0	394	19	US-09-503-089a-5
4	2042	100.0	394	20	US-09-655-272-5
5	1819	89.1	405	15	US-09-144-914-5
6	1819	89.1	405	18	US-09-436-265-5
7	1235.5	60.5	309	12	US-08-816-011C-55
8	1235.5	60.5	309	12	US-08-816-011C-62
9	1224	59.9	312	12	US-08-816-011-55
10	1224	59.9	312	12	US-08-816-011A-55

11	1116	54.7	374	19	US-09-516-279-1	Sequence 2, Appl1
12	1116	54.7	374	19	US-09-516-279-4	Sequence 4, Appl1
13	1116	54.7	374	23	US-60-199-020-2	Sequence 2, Appl1
14	846	41.4	400	19	US-09-518-866-1	Sequence 5, Appl1
15	838	41.0	400	19	US-09-518-866-1	Sequence 2, Appl1
16	838	41.0	400	23	US-60-203-495-1	Sequence 1, Appl1
17	777	38.1	339	23	US-60-161-932-1	Sequence 1980, Ap
18	777	38.1	340	23	US-60-167-245-1	Sequence 700, Ap
19	777	38.1	340	23	US-60-173-464-1	Sequence 16346, A
20	777	38.1	340	23	US-60-191-637-1	Sequence 19979, A
21	777	37.9	340	23	US-60-191-637-1	Sequence 15731, A
22	774	37.9	279	1	PCT-US01-00663	Sequence 27364, A
23	774	37.9	279	23	US-60-236-359-1	Sequence 15807, A
24	773	37.9	408	1	PCT-US00-20435	Sequence 12, Appl
25	773	37.9	408	17	US-09-362-842-1	Sequence 41787, A
26	742	36.3	398	23	US-60-191-637-1	Sequence 778, Ap
27	619.5	30.3	156	23	US-60-195-134	Sequence 776, Ap
28	615.5	30.1	126	23	US-60-195-134	Sequence 777, Ap
29	591.5	29.0	149	23	US-60-195-134	Sequence 479, Ap
30	475	23.3	170	23	US-60-142-843-1	Sequence 2599, Ap
31	455.5	22.3	101	23	US-60-196-712-1	Sequence 2595, Ap
32	453.5	22.2	101	23	US-60-196-712-1	Sequence 214, Ap
33	441.5	21.6	161	23	US-60-139-670-1	Sequence 529, Ap
34	441.5	21.6	161	23	US-60-140-804-1	Sequence 529, Ap
35	437	21.4	205	23	US-60-143-874-1	Sequence 250, Ap
36	432	21.2	114	23	US-60-170-429-1	Sequence 837, Ap
37	427	20.9	110	23	US-60-182-568-1	Sequence 957, Ap
38	414.5	20.3	101	23	US-60-196-712-1	Sequence 2597, Ap
39	382	18.7	102	23	US-60-196-712-1	Sequence 2598, Ap
40	381	18.7	102	23	US-60-196-712-1	Sequence 14, Appl
41	379	18.6	361	1	PCT-US00-20439-1	Sequence 14, Appl
42	379	18.6	361	17	US-09-362-842-1	Sequence 714, Appl
43	372	18.2	98	23	US-60-182-076-1	Sequence 8, Appl1
44	370	18.1	370	15	US-09-144-914-4	Sequence 8, Appl1
45	370	18.1	370	18	US-09-436-265-4	

ALIGNMENTS

RESULT 1

US-09-144-914-4

Sequence 4, Application US/09144914

GENERAL INFORMATION:

APPLICANT: Duprat, Florice

APPLICANT: Lesage, Florian

APPLICANT: Fink, Michel

APPLICANT: Lazdunski, Michel

TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING

TITLE OF INVENTION: AND THEIR USE, ESPECIALLY IN THE SCREENING OF DRUGS

FILE REFERENCE: 989.6705CIP

CURRENT APPLICATION NUMBER: US/09/144,914

CURRENT FILING DATE: 1998-09-01

EARLIER APPLICATION NUMBER: 08/7749,816

EARLIER FILING DATE: 1996-11-15

EARLIER APPLICATION NUMBER: 60/095,234

EARLIER FILING DATE: 1998-08-04

EARLIER APPLICATION NUMBER: FR 96/01565

EARLIER FILING DATE: 1996-02-08

NUMBER OF SEQ ID NOS: 24

SOFTWARE: Patentln Ver. 2.0

SEQ ID NO 4

LENGTH: 394

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: TASK

US-09-144-914-4

Query Match 100.0% Score 2042; Length 394;

Best Local Similarity 100.0%; Pred. No. 1;

Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[illegible]

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RESULT 2
US-09-436-265-4
: Sequence 4, Application US/09436265
: GENERAL INFORMATION:
: APPLICANT: REYES, ROBERTO
: APPLICANT: DUPRAT, FABRICE
: APPLICANT: LESAGE, FLOIRIAN
: APPLICANT: PINK, MICHEL
: APPLICANT: SALINAS, MIGUEL
: APPLICANT: FARMAN, NICOLETTE
: APPLICANT: LAZDUNSKI, MICHEL
: TITLE OF INVENTION: NEW FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR
: TITLE OF INVENTION: CLONING AND THEIR USE, ESPECIALLY FOR THE SCREENING OF
: TITLE OF INVENTION: DRUGS
: FILE REFERENCE: 1201-CIP2-00
: CURRENT APPLICATION NUMBER: US/09/436,265
: CURRENT FILING DATE: 1999-11-08
: PRIOR APPLICATION NUMBER: 60/095,234
: PRIOR FILING DATE: 1998-08-04
: PRIOR APPLICATION NUMBER: 60/107,692
: PRIOR FILING DATE: 1996-11-09
: NUMBER OF SEQ ID NOS: 32
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 4
: LENGTH: 394
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: TASK
US-09-436-265-4

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[illegible]

QY	121	TLVMEOSIGEBINLVLYLLHBRACKGGMGRADVSMANW	180	PFESCI STLICGAAFSH	180
Db	121	TLVMEOSIGEBINLVLYLLHBRACKGGMGRADVSMANW	180	PFESCI STLICGAAFSH	180
QY	181	YEHMTFEOAYVYCEITLTITITIGEGDYVALOKDOALOTOPV	240	SPVYILTLGLTVIGAFLN	240
Db	181	YEHMTFEOAYVYCEITLTITITIGEGDYVALOKDOALOTOPV	240	SPVYILTLGLTVIGAFLN	240
QY	241	LVVLREPMTMNAEDDKRDAEHRHALLTRNGOGGGGGGSAH	300	DTASSTAAGGGGGRPNY	300
Db	241	LVVLREPMTMNAEDDKRDAEHRHALLTRNGOGGGGGGSAH	300	DTASSTAAGGGGGRPNY	300
QY	301	AEVLHFOSMCSCLWYKSKREKLQVSIPIPIPRDLSTDPY	360	SHSHPGGGGRYSDTPSR	360
Db	301	AEVLHFOSMCSCLWYKSKREKLQVSIPIPIPRDLSTDPY	360	SHSHPGGGGRYSDTPSR	360
QY	361	CLGCGAPRSALTSVSTGLHSLSTRGMLMKRRSSV	394		
Db	361	CLGCGAPRSALTSVSTGLHSLSTRGMLMKRRSSV	394		

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RESULT 3
US-09-503-089A-5
Sequence 5, Application US/09503089A
GENERAL INFORMATION:
APPLICANT: PATEL, AMANDA J.
APPLICANT: HONORE, ERIC
APPLICANT: LESAGE, FLORIAN
APPLICANT: ROMEY, GEORGES
APPLICANT: LAZDUSKI, MICHEL
TITLE OF INVENTION: A method for the identification of anesthetics
FILE REFERENCE: fl1b12priv3-humanatREK
CURRENT APPLICATION NUMBER: US/09/503,089A
CURRENT FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Microsoft Word 2000
SEQ ID NO 5
LENGTH: 394
TYPE: PRF
ORGANISM: Mus sp.
FEATURE:
OTHER INFORMATION: TASK
US-09-503-089A-5

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Query Match	Similarity	100.0%	Score 2042	Pos 19	Length 354
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					Gaps
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Dp	1	MKROVRLTALIVCFYTLVGVAAFDALSESEPLEIE	LRQELRLRLRLSOGGE	60	
QY	61	ELERVVLRLKPKKAGVQWRFGSFFATVTTTIGYGI	TTDGGKVPQMFYALLGIDL	120	
Dp	61	ELERVVLRLKPKKAGVQWRFGSFFATVTTTIGYGH	TTDGGKVFQMFYALLGIDL	120	
QY	121	TLVVMOSIGERNITLVRLLTHRAKKGLDMRDVSMANN	IGFSCSITSLICIGAAASH	180	
Dp	121	TLVVMOSIGERNITLVRLLTHRAKKGLDMRDVSMANNV	IGFSCSITSLICIGAAASH	180	
QY	181	YEHMTFQAYYYCFTLTTLTIGFGDVVALQKDALOTOPQ	YFSSVYVLTLTGLTVIGAFLN	240	
Dp	181	YEHMTFQAYYYCFTLTTLTIGFGDVVALQKDALOTOPQ	YFSSVYVLTLTGLTVIGAFLN	240	
QY	241	LVLVLEFMTMNAEDEKRDAREHRLALLTRNGOAGGGGGGSAH	TDVASSSTPAAGGGGFRRNY	300	
Dp	241	LVLVLEFMTMNAEDEKRDAREHRLALLTRNGOAGGGGGSAH	DTVASSSTPAAGGGGFRRNY	300	
QY	301	AEVLHFQSMGCLWAKSKSEKLOYSTPMTIIPRLSTSDPC	SHSSPGGGGYSTPTPSRR	360	
Dp	301	AEVLHFQSMGCLWAKSKSEKLOYSTPMTIIPRLSTSDTVE	SHSSPGGGGYSTPTPSRR	360	



QY 361 CLCGAPRAISSVSTGLHSLSTFRGLMKRRSSV 394  
 Db 361 CLCGAPRAISSVSTGLHSLSTFRGLMKRRSSV 394

## RESULT 4

US-09-655-272-5  
 ; Sequence 5, Application US/09655272  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HONORE, ERIC  
 ; APPLICANT: FINK, MICHEL  
 ; APPLICANT: LAZDUNSKI, MICHEL  
 ; APPLICANT: LESAGE, FLORIAN  
 ; APPLICANT: DUPRAT, FABRICE  
 ; TITLE OF INVENTION: MECHANOSENSITIVE MAMMALIAN POTASSIUM CHANNELS  
 ; TITLE OF INVENTION: ACTIVATABLE BY POLYUNSATURATED FATTY ACIDS AND THE USE  
 ; TITLE OF INVENTION: OF SAID CHANNELS IN DRUG SCREENING  
 ; FILE REFERENCE: 1383-00  
 ; CURRENT APPLICATION NUMBER: US/09/655, 272  
 ; CURRENT FILING DATE: 2000-09-05  
 ; PRIOR APPLICATION NUMBER: PCT/FR99/00404  
 ; PRIOR FILING DATE: 1999-02-23  
 ; PRIOR APPLICATION NUMBER: FR 98/02725  
 ; PRIOR FILING DATE: 1998-03-05  
 ; NUMBER OF SEQ ID NOS: 5  
 ; SOFTWARE: Patentln Ver. 2.1  
 ; SEQ ID NO 5  
 ; LENGTH: 394  
 ; TYPE: PRT  
 ; ORGANISM: Unknown Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of unknown sequence: TASK  
 US-09-655-272-5

IFN

Query Match 100.0%; Score 2042; DB 20; Length 394;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-197;  
 Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKRONVTLIVCTFTYLLVGAAVFDALSEPTELROBLERQLELRARVNLSSGGYE 60  
 Db 1 MKRONVTLIVCTFTYLLVGAAVFDALSEPTELROBLERQLELRARVNLSSGGYE 60  
 QY 61 ELERVVLRLPKHAGVQWRFAGSFYFAITVITIGYHAPSTIDGKVFQMFYALLGPI 120  
 Db 61 ELERVVLRLPKHAGVQWRFAGSFYFAITVITIGYHAPSTIDGKVFQMFYALLGPI 120  
 QY 121 TLVWFOGLGRINTLVYLLHRAKKGIGMRADVSMANMVLIGFSCISTLCIGAAAFSH 180  
 Db 121 TLVWFOGLGRINTLVYLLHRAKKGIGMRADVSMANMVLIGFSCISTLCIGAAAFSH 180  
 QY 121 TLVWFOGLGRINTLVYLLHRAKKGIGMRADVSMANMVLIGFSCISTLCIGAAAFSH 180  
 Db 121 TLVWFOGLGRINTLVYLLHRAKKGIGMRADVSMANMVLIGFSCISTLCIGAAAFSH 180  
 QY 181 YEHMTFFQAYVYCFITLTITGFDYVALQKDALQTOPVAVSFYVILGLTVIGAFNL 240  
 Db 181 YEHMTFFQAYVYCFITLTITGFDYVALQKDALQTOPVAVSFYVILGLTVIGAFNL 240  
 QY 241 LVVLRFTMAAEDEKRDRAERHALLTRNGOAGGGGSAHTTDTASSTAAGGGGFNNY 300  
 Db 241 LVVLRFTMAAEDEKRDRAERHALLTRNGOAGGGGSAHTTDTASSTAAGGGGFNNY 300  
 QY 241 LVVLRFTMAAEDEKRDRAERHALLTRNGOAGGGGSAHTTDTASSTAAGGGGFNNY 300  
 Db 241 LVVLRFTMAAEDEKRDRAERHALLTRNGOAGGGGSAHTTDTASSTAAGGGGFNNY 300  
 QY 301 AEVLHFOSMCSCLMYKSREKLOYSIPIIPDLSTDTCEVQSHSSPGGGRYSDFPSRR 360  
 Db 301 AEVLHFOSMCSCLMYKSREKLOYSIPIIPDLSTDTCEVQSHSSPGGGRYSDFPSRR 360  
 QY 361 CLCGAPRAISSVSTGLHSLSTFRGLMKRRSSV 394  
 Db 361 CLCGAPRAISSVSTGLHSLSTFRGLMKRRSSV 394

## RESULT 5

US-09-144-914-5  
 ; Sequence 5, Application US/09144914  
 ; GENERAL INFORMATION:

APPLICANT: Duprat, Fabrice  
 APPLICANT: Lesage, Florian  
 APPLICANT: Fink, Michel  
 APPLICANT: Lazdunski, Michel  
 TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING  
 TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS  
 FILE REFERENCE: 989.6705CIP  
 CURRENT APPLICATION NUMBER: US/09/144, 914  
 CURRENT FILING DATE: 1998-09-01  
 EARLIER APPLICATION NUMBER: 08/749, 816  
 EARLIER FILING DATE: 1996-11-15  
 EARLIER APPLICATION NUMBER: 60/095, 234  
 EARLIER FILING DATE: 1998-08-04  
 EARLIER APPLICATION NUMBER: FR 96/01565  
 EARLIER FILING DATE: 1996-02-08  
 NUMBER OF SEQ ID NOS: 24  
 SOFTWARE: Patentln Ver. 2.0  
 SEQ ID NO 5  
 LENGTH: 405  
 TYPE: PRT  
 ORGANISM: Murine  
 FEATURE:  
 OTHER INFORMATION: TASK  
 US-09-144-914-5

Query Match 89.1%; Score 1819; DB 17; Length 405;  
 Best Local Similarity 88.1%; Pred. No. 7.6e-175;  
 Matches 357; Conservative 9; Mismatches 2; Indels 14; Gaps 2;

QY 4 QNVFTLIVCTFTYLLVGAAVFDALSEPTELROBLERQLELRARVNLSSGGYE 63  
 Db 1 ENVTALLIVCTFTYLLVGAAVFDALSEPTELROBLERQLELRARVNLSSGGYE 60  
 QY 64 RYVLRRLPKHAGVQWRFAGSFYFAITVITIGYHAPSTIDGKVFQMFYALLGPI 123  
 Db 61 RYVLRRLPKHAGVQWRFAGSFYFAITVITIGYHAPSTIDGKVFQMFYALLGPI 120  
 QY 124 MFOGLGRINTLVYLLHRAKKGIGMRADVSMANMVLIGFSCISTLCIGAAAFSHYEH 183  
 Db 121 MFOGLGRINTLVYLLHRAKKGIGMRADVSMANMVLIGFSCISTLCIGAAAFSHYEH 180  
 QY 184 WTEFQAYVYCFITLTITGFDYVALQKDALQTOPVAVSFYVILGLTVIGAFNLV 243  
 Db 181 WTEFQAYVYCFITLTITGFDYVALQKDALQTOPVAVSFYVILGLTVIGAFNLV 240  
 QY 244 LRFPTMAAEDEKRDRAERHALLTRNGOAGGGGSAHTTDTASSTAAGGGGV 291  
 Db 241 LRFPTMAAEDEKRDRAERHALLTRNGOAGGGGSAHTTDTASSTAAGGGGV 300  
 QY 292 -GGGGRNNYAEVLHFOSMCSCLMYKSREKLOYSIPIIPDLSTDTCEVQSHSSPGG 349  
 Db 301 GVGSGGRNNYAEVLHFOSMCSCLMYKSREKLOYSIPIIPDLSTDTCEVQSHSSPGG 360  
 QY 350 GGRYDTPSRCLCGAPRAISSVSTGLHSLSTFRGLMKRRSSV 394  
 Db 361 GGRYDTPSRCLCGAPRAISSVSTGLHSLSTFRGLMKRRSSV 394

## RESULT 6

US-09-436-265-5  
 ; Sequence 5, Application US/09436265  
 ; GENERAL INFORMATION:  
 ; APPLICANT: REYES, ROBERTO  
 ; APPLICANT: DUPRAT, FABRICE  
 ; APPLICANT: LESAGE, FLORIAN  
 ; APPLICANT: FINK, MICHEL  
 ; APPLICANT: SALINAS, MIGUEL  
 ; APPLICANT: FARMAN, NICOLETTE  
 ; APPLICANT: LAZDUNSKI, MICHEL  
 ; TITLE OF INVENTION: NEW FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR  
 ; TITLE OF INVENTION: CLONING AND THEIR USE, ESPECIALLY FOR THE SCREENING OF  
 ; TITLE OF INVENTION: DRUGS

```

; FILE REFERENCE: 1201-CIP2-00
; CURRENT APPLICATION NUMBER: US/09/436,265
; CURRENT FILING DATE: 1999-11-08
; PRIOR APPLICATION NUMBER: 60/095,234
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/107,692
; PRIOR FILING DATE: 1996-11-09
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 5
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Murine sp.
; FEATURE:
; OTHER INFORMATION: TASK
US-09-436-265-5

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Query Match      89.1%; Score 1819; DB 18; Length 405;
Best Local Similarity 88.1%; Pred. No. 7,6e-175;
Matches 357; Conservative 9; Mismatches 25; Indels 14; Gaps 2;

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QY 4 QNVRTALIVCTFTYLLVGAADFALDSEPELIERORLELRQDELRLARYNLSSGGYEEL 63
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DB 1 ENVRTALIVCTFTYLLVGAADFALDSEPELIERORLELRQDELRLARYNLSSGGYEEL 60
QY 64 RVLRLKPKAGVQWRFAGSFYFAITVITTTIGYGHAPSTDGKVCMEFYALLGIPLTLY 123
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DB 61 RVLRLKPKAGVQWRFAGSFYFAITVITTTIGYGHAPSTDGKVCMEFYALLGIPLTLY 120
QY 124 MPOSIGERINTVRLYLHRAKGLGMRADVMANVLLIGFSCISTLCIGAASFYHER 183
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DB 121 MPOSIGERINTVRLYLHRAKGLGMRADVMANVLLIGFSCISTLCIGAASFYHER 180
QY 184 WFFFOAYYYCFTLTITIGGDYVALOKDQALOTOPQYVAFSPYITLTGLTVGAFPLNLY 243
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DB 181 WFFFOAYYYCFTLTITIGGDYVALOKDQALOTOPQYVAFSPYITLTGLTVGAFPLNLY 240
QY 244 LRFMTMNAEDEKRDARHALLTRNGAGAGGGG-----GSAHTTDTASSTPAA----- 291
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 241 LRFMTMNAEDEKRDARHALLTRNGAGAGGGG-----GSAHTTDTASSTPAA----- 290
QY 292 --GGGGRNRYAEVLHFGQSCSLMYKSRKLYSIPMTIPRDLSTSDTCVESHSPGG 349
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 301 GVGSGGRNRYAEVLHFGQSCSLMYKSRKLYSIPMTIPRDLSTSDTCVESHSPGG 360
QY 350 GGRYSDTPSPHCLSGTORSALSSVSTGLHSLSTFRGLMKRRSSV 394
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 361 GGRYSDTPSPHCLSGTORSALSSVSTGLHSLSTFRGLMKRRSSV 405

```

```

RESULT 7
US-08-816-011C-55
; Sequence 55, Application US/08816011C
; GENERAL INFORMATION:
; APPLICANT: Pausch, Mark H
; TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,
; FILE REFERENCE: 01142, 0122 SEQUENCE LISTING
; CURRENT APPLICATION NUMBER: US/08/816,011C
; PRIOR FILING DATE: 1997-03-11
; PRIOR APPLICATION NUMBER: 08/332,312
; PRIOR FILING DATE: 1994-10-31
; PRIOR APPLICATION NUMBER: PCT/US95/14364
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Mus musculus
US-08-816-011C-55

```

```

; FILE REFERENCE: 1201-CIP2-00
; CURRENT APPLICATION NUMBER: US/09/436,265
; CURRENT FILING DATE: 1999-11-08
; PRIOR APPLICATION NUMBER: 60/095,234
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/107,692
; PRIOR FILING DATE: 1996-11-09
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 5
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Murine sp.
; FEATURE:
; OTHER INFORMATION: TASK
US-09-436-265-5

```

```

Query Match      60.5%; Score 1235.5; DB 12; Length 309;
Best Local Similarity 83.9%; Pred. No. 6.7e-116;
Matches 250; Conservative 8; Mismatches 27; Indels 13; Gaps 3;

```

```

QY 4 QNVRTALIVCTFTYLLVGAADFALDSEPELIERORLELRQDELRLARYNLSSGGYEEL 63
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 13 ENVRTALIVCTFTYLLVGAADFALDSEPELIERORLELRQDELRLARYNLSSGGYEEL 72
QY 64 RVLRLKPKAGVQWRFAGSFYFAITVITTTIGYGHAPSTDGKVCMEFYALLGIPLTLY 123
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 73 RVLRLKPKAGVQWRFAGSFYFAITVITTTIGYGHAPSTDGKVCMEFYALLGIPLTLY 132
QY 124 MPOSIGERINTVRLYLHRAKGLGMRADVMANVLLIGFSCISTLCIGAASFYHER 183
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 133 MPOSIGERINTVRLYLHRAKGLGMRADVMANVLLIGFSCISTLCIGAASFYHER 192
QY 184 WFFFOAYYYCFTLTITIGGDYVALOKDQALOTOPQYVAFSPYITLTGLTVGAFPLNLY 241
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 193 WFFFOAYYYCFTLTITIGGDYVALOKDQALOTOPQYVAFSPYITLTGLTVGAFPLNLY 249
QY 242 VVLRFTMNAEDEKRDARHALLTRNGAGAGGGG-----GSAHTTDTASSTPAA----- 291
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 250 VVLRFTMNAEDEKRDARHALLTRNGAGAGGGG-----GSAHTTDTASSTPAA----- 307

```

```

RESULT 8
US-08-816-011C-62
; Sequence 62, Application US/08816011C
; GENERAL INFORMATION:
; APPLICANT: Pausch, Mark H
; TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,
; FILE REFERENCE: 01142, 0122 SEQUENCE LISTING
; CURRENT APPLICATION NUMBER: US/08/816,011C
; PRIOR FILING DATE: 1997-03-11
; PRIOR APPLICATION NUMBER: 08/332,312
; PRIOR FILING DATE: 1994-10-31
; PRIOR APPLICATION NUMBER: PCT/US95/14364
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Mus musculus
US-08-816-011C-62

```

```

QY 4 QNVRTALIVCTFTYLLVGAADFALDSEPELIERORLELRQDELRLARYNLSSGGYEEL 63
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 13 ENVRTALIVCTFTYLLVGAADFALDSEPELIERORLELRQDELRLARYNLSSGGYEEL 72
QY 64 RVLRLKPKAGVQWRFAGSFYFAITVITTTIGYGHAPSTDGKVCMEFYALLGIPLTLY 123
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 73 RVLRLKPKAGVQWRFAGSFYFAITVITTTIGYGHAPSTDGKVCMEFYALLGIPLTLY 132
QY 124 MPOSIGERINTVRLYLHRAKGLGMRADVMANVLLIGFSCISTLCIGAASFYHER 183
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 133 MPOSIGERINTVRLYLHRAKGLGMRADVMANVLLIGFSCISTLCIGAASFYHER 192
QY 184 WFFFOAYYYCFTLTITIGGDYVALOKDQALOTOPQYVAFSPYITLTGLTVGAFPLNLY 241
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 193 WFFFOAYYYCFTLTITIGGDYVALOKDQALOTOPQYVAFSPYITLTGLTVGAFPLNLY 249
QY 242 VVLRFTMNAEDEKRDARHALLTRNGAGAGGGG-----GSAHTTDTASSTPAA----- 291
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

Db 250 VLVLFMTNNADEKRDADHRLALTHNGQAVGLGSLGSLGDCVPRDPVTCAAA 307

## RESULT 9

US-08-816-011-55

; Sequence 55, Application US/08816011

; GENERAL INFORMATION:

; APPLICANT: Price, Laura A.

; APPLICANT: Pausch, Mark H.

; TITLE OF INVENTION: Potassium Channels, Nucleotide Sequences

; TITLE OF INVENTION: Encoding Them, and Methods of Using Same

; NUMBER OF SEQUENCES: 56

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: American Home Products Corporation

; STREET: One Campus Drive

; CITY: Parsippany

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07054

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/816,011

; FILING DATE: 11-MAR-1997

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: Matthews, Gale F.

; REGISTRATION NUMBER: 32,269

; REFERENCE/DOCKET NUMBER: 32,421-C2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-683-2134

; TELEFAX: 201-683-4117

; INFORMATION FOR SEQ ID NO: 55:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 312 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-816-011-55

Query Match 59.9% Score 1224 DB 12 Length 312;

Best Local Similarity 83.1% Pred. No. 9.9e-115;

Matches 250; Conservative 8; Mismatches 27; Indels 16; Gaps 4;

Db 4 QNVRTLAIYCTFTYLLVGAVPDALESEPELIERORLELRQOELRAVNLSSGGYELE 63

Db 13 ENVRTLAIYCTFTYLLVGAVPDALESEPEMIRORLELRQOELRAVNLSSGGYELE 72

Db 64 RVLRLKPKHKGVMRRFAGSFYFAITVTTTIGYGAAPSTDGCV--FCMFYALLGIPL 120

Db 73 RVLRLKPKHKGVMRRFAGSFYFAITVTTTIGYGAAPSTDGCVFCMFYALLGIPL 132

Db 121 TLVVFQSLGERINTLVRLRLKRAKGLGMRADYMANMVLIGFSCISTLCIGAAAFSH 180

Db 133 TLVVFQSLGERINTSVRLRLKRAKGLGMRADYMANMVLIGFSCISTLCIGAAAFSY 192

Db 181 YEHMTFFQAYYYCFITLTITIGFDYVALQKDALOTOPQYVAFSFTVLTGLTYIG--AF 238

Db 193 YEHMTFFQAYYYCFITLTITIGFDYVALQKDALOTOPQYVAFSFTVLTGLTYIG--AF 249

Db 239 LNLVLRFTMTNNADEKRDADHRLALTRNGQAVGLGSLGSLGDCVPRDPVTCAAA 290

Db 250 LNLVLRFTMTNNADEKRDADHRLALTRNGQAVGLGSLGSLGDCVPRDPVTCAAA 309

QY 291 A 291

Db 310 A 310

## RESULT 10

US-08-816-011A-55

; Sequence 55, Application US/08816011A

; GENERAL INFORMATION:

; APPLICANT: Price, Laura A.

; APPLICANT: Pausch, Mark H.

; TITLE OF INVENTION: Potassium Channels, Nucleotide Sequences

; TITLE OF INVENTION: Encoding Them, and Methods of Using Same

; NUMBER OF SEQUENCES: 56

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: American Home Products Corporation

; STREET: One Campus Drive

; CITY: Parsippany

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07054

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/816,011A

; FILING DATE: 11-MAR-1997

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: Matthews, Gale F.

; REGISTRATION NUMBER: 32,269

; REFERENCE/DOCKET NUMBER: 32,421-C2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-683-2134

; TELEFAX: 201-683-4117

; INFORMATION FOR SEQ ID NO: 55:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 312 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-816-011A-55

Query Match 59.9% Score 1224 DB 12 Length 312;

Best Local Similarity 83.1% Pred. No. 9.9e-115;

Matches 250; Conservative 8; Mismatches 27; Indels 16; Gaps 4;

Db 4 QNVRTLAIYCTFTYLLVGAVPDALESEPELIERORLELRQOELRAVNLSSGGYELE 63

Db 13 ENVRTLAIYCTFTYLLVGAVPDALESEPEMIRORLELRQOELRAVNLSSGGYELE 72

Db 64 RVLRLKPKHKGVMRRFAGSFYFAITVTTTIGYGAAPSTDGCV--FCMFYALLGIPL 120

Db 73 RVLRLKPKHKGVMRRFAGSFYFAITVTTTIGYGAAPSTDGCVFCMFYALLGIPL 132

Db 121 TLVVFQSLGERINTLVRLRLKRAKGLGMRADYMANMVLIGFSCISTLCIGAAAFSH 180

Db 133 TLVVFQSLGERINTSVRLRLKRAKGLGMRADYMANMVLIGFSCISTLCIGAAAFSY 192

Db 181 YEHMTFFQAYYYCFITLTITIGFDYVALQKDALOTOPQYVAFSFTVLTGLTYIG--AF 238

Db 193 YEHMTFFQAYYYCFITLTITIGFDYVALQKDALOTOPQYVAFSFTVLTGLTYIG--AF 249

Db 239 LNLVLRFTMTNNADEKRDADHRLALTRNGQAVGLGSLGSLGDCVPRDPVTCAAA 290

Db 250 LNLVLRFTMTNNADEKRDADHRLALTRNGQAVGLGSLGSLGDCVPRDPVTCAAA 309

QY 291 A 291

Db 310 A 310

## RESULT 11

US-09-516-279-2

; Sequence 2, Application US/09516279

```

: GENERAL INFORMATION:
: APPLICANT: David M. Duckworth
: APPLICANT: Robert J. Godden
: APPLICANT: Conrad G. Chapman
: APPLICANT: Helen J. Meadows
: TITLE OF INVENTION: NOVEL COMPOUNDS
: FILE REFERENCE: GP-30200
: CURRENT APPLICATION NUMBER: US/09/516,279
: CURRENT FILING DATE: 2000-03-01
: EARLIER APPLICATION NUMBER: UK 9905061.9
: EARLIER FILING DATE: 1999-03-05
: EARLIER APPLICATION NUMBER: UK 0003112.0
: EARLIER FILING DATE: 2000-02-09
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO 2
: LENGTH: 374
: TYPE: PR1
: ORGANISM: HOMO SAPIENS
: US-09-516-279-2

```

```

Query Match Summary          54.7%: Score 116: Db 19: Length 374:
Best Local Similarity       59.0%: Pred. No. 1.1e-103:
Matches 233: Conservative 44: Mismatches 96: Indels 22: Gaps 5

QY      1 MKRONVRLALIVCTFTYLLVGAAYFDALSEPELIERORLELRQOELRARNLSGGYE 60
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1 MKRONVRLTSLIVCTFTYLLVGAAYFDALSEHMEKEELKAEETIRIKGTYNISSEYR 60
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      61 ELERVLLKPKACVOMRFGSEFATVITVITTYGHAAPSTDGKVCMTALLGTL 120
      61 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      61 QELVLTQSEPRACVOMKFGSEFATVITVITTYGHAAPSTDGKACMTAVAVIGPL 120
      61 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      121 TLVPMQSGERINTLVRYLLHRAKKGIGMRADVSMANVLLGFEFSCIITLIGAAFSH 180
      121 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      121 TLVPMQSGERINTLVRYLLKIRKCCGMRNDVSMENNVYVGFSSCMETLCIGAAAFQ 180
      121 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      181 YEHMTFPOAYVYCFITLTITGFDVALQDQALOTPOPYAFSPVYILTGLTVIGAFNL 240
      181 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      181 CEEMFEPHAYVYCFITLTITGFDVALQTKALOKKPLXYAFSPWYILVGLTVIGAFNL 240
      181 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      241 LVVLEFMTNMNDEKRDDEHRLALLTRNQAAGGGGGGSHHTDITASSTAAAGGGRNVY 300
      241 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      241 LVVLEFMTNMSDERKDAEERASTL-----AANRSMVTHIPEEPPS-----RPRY 286
      241 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      301 -AEVLFPMQSMCSCLWYKREKRLQYISIPMLIPDLSTSDPTVCQSHSPGGGGRYSDPTPSR 359
      301 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      287 KADVDDLOSVCSCCTCYRSD---YGRSVAAPNPSAKLAIPHFIHSIKTIEISPTLK 343
      287 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      360 RCLCGAPRSAISSVSTGLHSLSTFRGLMKRRSSV 394
      360 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      344 NSLFP-----SPISISPGHSTFDHQRLMKRRKSV 374
      344 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 12
US-09-516-279-4
: Sequence 4, Application US/09516279
: GENERAL INFORMATION:
: APPLICANT: David M. Duckworth
: APPLICANT: Robert J. Godden
: APPLICANT: Conrad G. Chapman
: APPLICANT: Helen J. Meadows
: TITLE OF INVENTION: NOVEL COMPOUNDS
: FILE REFERENCE: GP-30200
: CURRENT APPLICATION NUMBER: US/09/516,279
: CURRENT FILING DATE: 2000-03-01
: EARLIER APPLICATION NUMBER: UK 9905061.9
: EARLIER FILING DATE: 1999-03-05
: EARLIER APPLICATION NUMBER: UK 0003112.0
: EARLIER FILING DATE: 2000-02-09
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: FastSeq for Windows Version 3.0

```

```

; SEQ ID NO 4
; LENGTH: 374
; TYPE: prt
; ORGANISM: HOMO SAPIENS
US-09-516-279-4

```

[illegible]

```

RESULT 13
US-60-199-020-2
; Sequence 2, Application US/60199020
; GENERAL INFORMATION:
; APPLICANT: Sanjanwala, Madhu Sudan
; APPLICANT: Baughn, Mariah R.
; APPLICANT: Yao, Monique G.
; APPLICANT: Nguyen, Damien B.
; TITLE OF INVENTION: POLICY, Jennifer L.
; FILE REFERENCE: PI-0073 P
; CURRENT APPLICATION NUMBER: US/60/199,020
; CURRENT FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PERL program
; SEQ ID NO 2
; LENGTH: 374
; TYPE: PRF
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 7472584CD1
US-60-199-020-2

```

```
Query Match      54.7%  Score 1116.  DB 1.3  Length 374;
Best Local Similarity 59.0%  Pred. No. 1.1e+05
Matches 233; Conservative 44; Mismatches 94; Indels 22; Gaps 5;

OY 1 MKRONVTLALIVCTFFTYLLVGAAFDALSPELIEROFN...ROOELRARNYSOGYE 60
    |||||.....
    |||||.....
1 MKRONVTLALIVCTFFTYLLVGAAFDALSDEHREERKKAETIRKGVNISSEYR 60
    |||||.....
```





GenCore version 4.5  
Copyright (c) 1993 - 2000 Comugen Ltd.

OM protein - protein search, using sw model

Run on: August 28, 2001, 17:11:45 ; Search time 24.66 Seconds  
(without alignments)  
342.699 Million cell updates/sec

Title: US-09-503-089a-5  
Perfect score: 2042  
Sequence: 1 MKRONVRLALIVCTFTYLL.....STGLHSLSTFRQIMKRSSV 394

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 154674 seqs, 21449152 residues

Total number of hits satisfying chosen parameters: 154674

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Pending\_Patents\_AA\_New:\*  
1: /cgn2\_6/ptodata/1/paa/PCT\_NEW\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/paa/US06\_NEW\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/paa/US07\_NEW\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/paa/US60\_NEW\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2042	100.0	394	US-09-798-584-15	Sequence 15, App1
2	1278	62.6	258	US-09-746-491-61	Sequence 61, App1
3	1116	54.7	374	US-09-798-584-1	Sequence 1, App1
4	1069.5	52.4	365	US-09-746-491-60	Sequence 60, App1
5	846	41.4	330	US-09-746-491-59	Sequence 59, App1
6	838	41.0	330	US-09-746-491-58	Sequence 58, App1
7	838	41.0	330	US-09-746-491-22	Sequence 22, App1
8	363	17.8	411	US-09-336-643-83	Sequence 83, App1
9	319	15.6	499	US-09-431-367B-2	Sequence 2, App1
10	295.5	14.5	313	US-09-431-367B-8	Sequence 8, App1
11	295.5	14.5	313	US-09-336-643-81	Sequence 81, App1
12	294.5	14.4	332	US-09-431-367B-5	Sequence 5, App1
13	251.5	12.3	401	US-09-431-367B-11	Sequence 11, App1
14	179	8.8	39	US-09-746-491-63	Sequence 63, App1
15	135.5	6.4	205	US-09-760-469-1386	Sequence 1386, App1
16	131.5	6.4	646	US-09-336-643-10	Sequence 10, App1
17	118	5.8	988	US-09-299-378-3	Sequence 3, App1
18	118	5.8	988	US-09-300-614-3	Sequence 3, App1
19	114	5.6	988	US-09-299-378-2	Sequence 2, App1
20	114	5.6	988	US-09-300-614-2	Sequence 2, App1
21	113.5	5.6	962	US-09-300-614-5	Sequence 5, App1
22	113.5	5.6	962	US-09-300-614-5	Sequence 5, App1
23	113.5	5.6	989	US-09-300-614-6	Sequence 6, App1
24	113.5	5.6	989	US-09-300-614-6	Sequence 6, App1
25	113	5.5	187	US-09-336-643-16	Sequence 16, App1
26	112.5	5.5	1082	US-09-336-643-20	Sequence 20, App1
27	111.5	5.5	962	US-09-299-378-4	Sequence 4, App1

28	111.5	5.5	962	US-09-300-614-4	Sequence 4, App1
29	111	5.4	947	US-09-304-243-2	Sequence 2, App1
30	111	5.4	994	US-09-304-243-8	Sequence 8, App1
31	103.5	5.1	950	US-09-304-243-9	Sequence 9, App1
32	102.5	5.0	221	US-09-299-378-2	Sequence 21, App1
33	102.5	5.0	221	US-09-300-614-2	Sequence 21, App1
34	98.5	4.8	200	US-09-760-469-1	Sequence 1063, App1
35	98.5	4.8	221	US-09-760-469-1	Sequence 1558, App1
36	98.5	4.8	222	PCT-US01-18569-1	Sequence 1268, App1
37	98.5	4.8	844	US-09-573-655A	Sequence 7, App1
38	98.5	4.8	1174	US-09-299-378-7	Sequence 7, App1
39	98.5	4.8	1174	US-09-300-614-7	Sequence 14, App1
40	97.5	4.8	289	US-09-372-422A	Sequence 10, App1
41	97.5	4.8	1195	US-09-304-243-1	Sequence 12, App1
42	95.5	4.7	282	US-09-372-422A	Sequence 6, App1
43	95.5	4.7	288	US-09-372-422A	Sequence 49, App1
44	94	4.6	254	US-09-304-243-1	
45	94	4.6	1159	US-09-299-378-1	

ALIGNMENTS

RESULT 1  
US-09-798-584-15  
; Sequence 15, Application US/09798584  
; GENERAL INFORMATION:  
; APPLICANT: Mu, David  
; APPLICANT: Powers, Scott  
; APPLICANT: Talarik Inc.  
; TITLE OF INVENTION: KCNB: A Novel Potassium  
; FILE REFERENCE: 018781-004010US  
; CURRENT APPLICATION NUMBER: US/09/798,584  
; PRIOR FILING DATE: 2001-03-03  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 15  
; LENGTH: 394  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: human potassium channel K<sub>v</sub>1.1 (TASK1)

us-09-503-089a-5.Aug28.rapn

Query Match 100.0%; Score 2042;  
Best Local Similarity 100.0%; Pred. No. 1.1;  
Matches 394; Conservative 0; Mismatches 0;

Length 394;  
Indels 0; Gaps 0;

QY	1	MKRONVRLALIVCTFTYLLVGAAVFDALSEPELIER	100ELRLRYNLSGGYE 60
DB	1	MKRONVRLALIVCTFTYLLVGAAVFDALSEPELIER	100ELRLRYNLSGGYE 60
QY	61	ELEFVRLKPKHKGVMRFAGSFYFAITVTTTGYG	100GKVFCEFYALGPI 120
DB	61	ELEFVRLKPKHKGVMRFAGSFYFAITVTTTGYG	100GKVFCEFYALGPI 120
QY	121	TLVFOSLGERINTLVRYLHRAKKGJMRADYSMA	100GKVFCEFYALGPI 120
DB	121	TLVFOSLGERINTLVRYLHRAKKGJMRADYSMA	100GKVFCEFYALGPI 120
QY	181	YEHTEFOAYYCCITLTGFGDYVALQKDALOTQ	100GKVFCEFYALGPI 120
DB	181	YEHTEFOAYYCCITLTGFGDYVALQKDALOTQ	100GKVFCEFYALGPI 120
QY	241	LVVLRFTMAEDKRDARHALLTRNGOAGGGGGS	100GKVFCEFYALGPI 120
DB	241	LVVLRFTMAEDKRDARHALLTRNGOAGGGGGS	100GKVFCEFYALGPI 120
QY	301	AEVLHFSQSCSLWYKSRKQYSIPMIIPDLSTST	100GKVFCEFYALGPI 120
DB	301	AEVLHFSQSCSLWYKSRKQYSIPMIIPDLSTST	100GKVFCEFYALGPI 120

Db 301 AEVLHQMCSCLMYSREKLYSIPMIIPDLSTSDTVEOSHSPGGGGRYSDTPSR 360  
 QY 361 CLCGAPRSAISSVSTGLHSLSTFRGLMKRRSSV 394  
 Db 361 CLCGAPRSAISSVSTGLHSLSTFRGLMKRRSSV 394

RESULT 2  
 US-09-746-491-61  
 ; Sequence 61, Application US/09746491  
 ; GENERAL INFORMATION:

; APPLICANT: Burgess, Catherine E.  
 ; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same  
 ; FILE REFERENCE: 15966-621  
 ; CURRENT APPLICATION NUMBER: US/09/746,491  
 ; CURRENT FILING DATE: 2000-12-20  
 ; PRIOR APPLICATION NUMBER: USSN 60/171,329  
 ; PRIOR FILING DATE: 1999-12-21  
 ; NUMBER OF SEQ ID NOS: 72  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 61  
 ; LENGTH: 258  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 US-09-746-491-61

Query Match 62.6%; Score 1278; DB 5; Length 258;  
 Best Local Similarity 96.1%; Pred. No. 58e-108;  
 Matches 248; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 MKRONVRLTALIVCTFTYLLVGAADFALDESEBELIERORLEIROELRARNYLSOGGYE 60  
 Db 1 MKRONVRLTALIVCTFTYLLVGAADFALDESEBELIERORLEIROELRARNYLSOGGYE 60  
 QY 61 ELERVYLRKPKHAGVQMPAGSFYFAITVITTTIGYGHAPSTDGKVCMPFALLGIP 120  
 Db 61 ELERVYLRKPKHAGVQMPAGSFYFAITVITTTIGYGHAPSTDGKVCMPFALLGIP 120  
 QY 121 TLVMPQSLGERINTLVRYLLHRAKGLGRRADVSMAWVLTGFFSCISTLCIGAASFH 180  
 Db 121 TLVMPQSLGERINTLVRYLLHRAKGLGRRADVSMAWVLTGFFSCISTLCIGAASFH 180  
 QY 181 YEHMTFFQAYVYCFITLTTIGFGDYVALOKDQALQTOPQYVAFSEFYILTGLTVIGAFIN 240  
 Db 181 YEHMTFFQAYVYCFITLTTIGFGDYVALOKDQALQTOPQYVAFSEFYILTGLTVIGAFIN 240  
 QY 241 LVLRPMTNMADEKRD 258  
 Db 241 LVLRPMTNMADEKRD 258

RESULT 3  
 US-09-798-584-1  
 ; Sequence 1, Application US/09798584  
 ; GENERAL INFORMATION:

; APPLICANT: Mu, David  
 ; APPLICANT: Powers, Scott  
 ; APPLICANT: Tularik Inc.  
 ; TITLE OF INVENTION: A Novel Potassium Channel Protein  
 ; FILE REFERENCE: 018781-004010US  
 ; CURRENT APPLICATION NUMBER: US/09/798,584  
 ; CURRENT FILING DATE: 2001-03-03  
 ; PRIOR APPLICATION NUMBER: US 60/186,951  
 ; PRIOR FILING DATE: 2000-03-03  
 ; NUMBER OF SEQ ID NOS: 18  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 1  
 ; LENGTH: 374  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 OTHER INFORMATION: human KCNB (Potassium Channel expressed in Breast)

US-09-798-584-1

Query Match 54.7%; Score 1116; DB 5; Length 374;  
 Best Local Similarity 59.0%; Pred. No. 3.9e-93;  
 Matches 233; Conservative 44; Mismatches 9; Indels 22; Gaps 5;

QY 1 MKRONVRLTALIVCTFTYLLVGAADFALDESEBELIERORLEIROELRARNYLSOGGYE 60  
 Db 1 MKRONVRLTALIVCTFTYLLVGAADFALDESEBELIERORLEIROELRARNYLSOGGYE 60  
 QY 61 ELERVYLRKPKHAGVQMPAGSFYFAITVITTTIGYGHAPSTDGKVCMPFALLGIP 120  
 Db 61 ELERVYLRKPKHAGVQMPAGSFYFAITVITTTIGYGHAPSTDGKVCMPFALLGIP 120  
 QY 121 TLVMPQSLGERINTLVRYLLHRAKGLGRRADVSMAWVLTGFFSCISTLCIGAASFH 180  
 Db 121 TLVMPQSLGERINTLVRYLLHRAKGLGRRADVSMAWVLTGFFSCISTLCIGAASFH 180  
 QY 181 YEHMTFFQAYVYCFITLTTIGFGDYVALOKDQALQTOPQYVAFSEFYILTGLTVIGAFIN 240  
 Db 181 YEHMTFFQAYVYCFITLTTIGFGDYVALOKDQALQTOPQYVAFSEFYILTGLTVIGAFIN 240  
 QY 241 LVLRPMTNMADEKRDALHRLALTRNGOAGGGGGSAACTAATAAGGGGRNVY 300  
 Db 241 LVLRPMTNMADEKRDALHRLALTRNGOAGGGGGSAACTAATAAGGGGRNVY 300  
 QY 301 AEVLHQMCSCLMYSREKLYSIPMIIPDLSTSDTVEOSHSPGGGGRYSDTPSR 359  
 Db 287 KADVPDQVSCCTCYRSD---YGRSAVAPONSASAKLAPVFNSTVYKIEIISPTLK 343  
 QY 360 KCLCGAPRSAISSVSTGLHSLSTFRGLMKRRSSV 394  
 Db 344 NSLFP---SPISISPLGHSFTDQRLMKRRSV 374

RESULT 4  
 US-09-746-491-60  
 ; Sequence 60, Application US/09746491  
 ; GENERAL INFORMATION:

; APPLICANT: Burgess, Catherine E.  
 ; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same  
 ; FILE REFERENCE: 15966-621  
 ; CURRENT APPLICATION NUMBER: US/09/746,491  
 ; CURRENT FILING DATE: 2000-12-20  
 ; PRIOR APPLICATION NUMBER: USSN 60/171,329  
 ; PRIOR FILING DATE: 1999-12-21  
 ; NUMBER OF SEQ ID NOS: 72  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 60  
 ; LENGTH: 365  
 ; TYPE: PRT  
 ; ORGANISM: Cavia porcellus  
 US-09-746-491-60

Query Match 52.4%; Score 1069.5; DB 5; Length 365;  
 Best Local Similarity 57.1%; Pred. No. 6e-84;  
 Matches 226; Conservative 43; Mismatches 9; Indels 33; Gaps 6;

QY 1 MKRONVRLTALIVCTFTYLLVGAADFALDESEBELIERORLEIROELRARNYLSOGGYE 60  
 Db 1 MKRONVRLTALIVCTFTYLLVGAADFALDESEBELIERORLEIROELRARNYLSOGGYE 60  
 QY 61 ELERVYLRKPKHAGVQMPAGSFYFAITVITTTIGYGHAPSTDGKVCMPFALLGIP 120  
 Db 61 ELERVYLRKPKHAGVQMPAGSFYFAITVITTTIGYGHAPSTDGKVCMPFALLGIP 120  
 QY 121 TLVMPQSLGERINTLVRYLLHRAKGLGRRADVSMAWVLTGFFSCISTLCIGAASFH 180  
 Db 121 TLVMPQSLGERINTLVRYLLHRAKGLGRRADVSMAWVLTGFFSCISTLCIGAASFH 180  
 QY 181 YEHMTFFQAYVYCFITLTTIGFGDYVALOKDQALQTOPQYVAFSEFYILTGLTVIGAFIN 240  
 Db 181 YEHMTFFQAYVYCFITLTTIGFGDYVALOKDQALQTOPQYVAFSEFYILTGLTVIGAFIN 240



[illegible]

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Query March 1970      41.4%: Score 846; DB 5; Length 330;
Best Local Similarity 64.7%; Pred. No. 7.9e-69;
Matches 167; Conservative 32; Mismatches 59; Indels 0; Gaps 0;

QY      1 MKRONVRLIALVCFTFFLLVGAAFDAALESEPELIERORLELRROEELRARRYLSQGGE 60
       1 : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1 MRPSVRAAGVLCTCLYLVGAAVFDALESAGEGRQLRVQRKGALRRKGFSAEDR 60
       1 : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      61 ELERVLRCLKPKAKGVQWRFAGSFEYFALTIVTTIGYGHAAPSTDGCKVFCMFYALLGIPL 120
       1 : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      61 ELERLALQAEPRHARGQKKFPQSFEYFALTIVTTIGYGHAAPSTDGCKVFCMFYALLGIPL 120
       1 : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      121 TLVMQSGISGERINTLYVRLLHRAKGGLGMRRADVSMANNVLTIGFSCLSTLCIGAANASH 180
       1 : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      121 TLYVFOSSIGERINAVVRRLTLAAMCCCLLRMTCVSTEMLVVAGLACATATLGGVAESH 180
       1 : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      181 YEHWTFQAYVYYCFETLTITGFGDVVALOKDOALTOPQYVAFSPVILTGLTVGAFNL 240
       1 : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      181 FEGWTFEFAYIYCFTLTLTITGFGDVVALQSGEALORKLPYAASFYLLTGLTVIGAFNL 240
       1 : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      241 LVVLFRTMNADEKERDA 258
       1 : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      241 LVVLFRLFVASADWPERRA 258
       1 : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT        6
US-09-746-491-58
Sequence 58, Application us/09746491
GENERAL INFORMATION:
APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 15966-621
CURRENT APPLICATION NUMBER: US/09/746,491
CURRENT FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: USSN 60/171,329
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 72

```

[illegible]

```

RESULT      7
US-09-746-491-22
; Sequence 22, Application US/09746491
; GENERAL INFORMATION:
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-621
; CURRENT APPLICATION NUMBER: US/09/746,491
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: USSN 60/171,329
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 393
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (340)
; OTHER INFORMATION: wherein xaa is any amino acid as defined in the
; OTHER INFORMATION: specification
US-09-746-491-22

Query Match          41.0%; Score 838; Dk %: Length 393;
Best Local Similarity   64.3%; Pred. No. 5.2e+04;
Matches    166; Conservative     32; Mismatches    59; Indels       0; Gaps        0.
```

```
QY 181 YEHWFEOAYYCFITLTITGGFDYVALOKDOALOTOPQYVAFSEFYILGLVIGAFNL 240
: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 FEGWTFPHAYYCFITLTITGGFDYVALOKDOALOTOPQYVAFSEFYILGLVIGAFNL 240
QY 241 LVVLRFTMNAEDEKRD 258
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 241 LVVLRFTMNAEDEKRD 258
```

## RESULT 8

```
US-09-336-643-83
; Sequence 83, Application US/09336643
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rutler, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: Novel Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/09/336,643
; CURRENT FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 411
; TYPE: PRT
; ORGANISM: H. sapiens
US-09-336-643-83
```

Query Match 17.8%; Score 363; DB 5; Length 411;

Best Local Similarity 31.0%; Pred. No. 4,2e-25;

Matches 91; Conservative 59; Mismatches 102; Indels 42; Gaps 9;

```
QY 1 MKRONVTLALVCTFTYLLVGAAPDALESEPELIERORLEROELRARNLSGGYE 60
: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 42 MKKVTSTILV--VYLIIIGATVFALQPHIEISQRTTIVIOKOTFISQHSVNS--T 97
61 ELEEVVRL-KPHKAGY-----QWRFGSEFEATVTTTIGGHAAPSTDGKV 108
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 98 ELDELIOQIVAAINAGIIPLGNTSNOISHWDLGSSFFFACTVTTTIGGHAAPSTDGKI 157
109 FCFEYALGIPILVMPGOSIGERINTLVRLHRAKKGIMRRAD-----VSM 156
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 158 FCIITVALGIPLEGFLLAGVGDQGTIF-----GKIAVEDTFIKMNSQTKIRI 208
157 ANNVLIGFESCITLCIGAAAFSHYEHWFEOAYYCFITLTITGGFDYVALOKDOALOT 216
: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 209 ISTIIFLFCVLEVALPFIIFKHIEGMSALDAIYEVVITLTITGGFDYVAGGSD--IEY 266
217 QPOYVAFSEFYILGLVIGAFNLV--VLRFMTMNAEDEKRD-AEIRALLTIN 267
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 267 LDYKPYVWMILVGLAFPAVLISMIGDWLRVSKTKKEEVGEERAAHAEWTAN 320
```

## RESULT 9

```
US-09-431-367B-2
; Sequence 2, Application US/09431367B
; GENERAL INFORMATION:
; APPLICANT: Cutlis, Roy A. J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-074CP
; CURRENT APPLICATION NUMBER: US/09/431,367B
; CURRENT FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: 09/259,951
```

```
; PRIOR FILING DATE: 1999-03-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 2
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-431-367B-2
```

Query Match 15.6%; Score 319; DB 5; Length 499;

Best Local Similarity 32.8%; Pred. No. 5e-21;

Matches 84; Conservative 47; Mismatches 9; Indels 28; Gaps 8;

```
QY 18 YLVGAAPDALESEPELIERORLEROELRARNLSGGYEELERV----- 66
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 15 YLAIGAIFEVLE-EPHWKRAKNYYTOKLHL---LRF-IGOEGLDILLEVSDAG 69
67 --LRKPKAGVQWRFAGSEFYAITVTTTIGGHAAPS--AVFCMFYALGIPILVM 124
: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 70 QGVAITGNQTFNNMNMNMAIFATVTTTIGGVNAPK--KLFVYGLFVGLCTW 129
QY 125 FQSLGE---RINTLVRYLLHRAKKGIMRRADVSMAN--FFSCISTLCIGAAAFSH 180
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 130 ISALGKFFGGRAKRLGQFL--TKRGVSLRKAQITCTV--WGVLVHLVIPPEFVW 184
QY 181 YEHWFEOAYYCFITLTITGGFDYVALOKDOALOTOPQYVAFSEFYILGLVIGAFNL 240
: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 185 TEGNNTIEGLYSPITLTITGGFDYVAGVNPNA-NHHA--FVELMTYILGLMLSLEVN 243
QY 241 LVVLRFTMNAEDEKR 256
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 244 WKVSMFEYVHKAIKKR 259
```

## RESULT 10

```
US-09-431-367B-8
; Sequence 8, Application US/09431367B
; GENERAL INFORMATION:
; APPLICANT: Cutlis, Roy A. J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-074CP
; CURRENT APPLICATION NUMBER: US/09/431,367B
; CURRENT FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: 09/259,951
; PRIOR FILING DATE: 1999-03-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 8
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-431-367B-8
```

Query Match 14.5%; Score 295.5; Length 313;

Best Local Similarity 31.7%; Pred. No. 3.7e-15;

Matches 90; Conservative 40; Mismatches 15; Indels 59; Gaps 12;

```
QY 18 YLVGAAPDALESEPELIERORLEROELRARNLSGGYEELERV-----LSGGYEEL 63
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 17 YLVGALLVARLEGPHEARLRALETLRAOLLORSPCY--LDAFVERVLAAG---RLG 73
QY 64 RYVLRKLPKAGVQ--WRFAGSEFYAITVTTTIGGHAAPS--AVFCMFYALGIPILVM 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 74 RYVLANSSGASANDPAMDASALFPASTLTITVGVY--IDACKRAFSIAFALLGVPL 133
QY 121 TLVMPGOSIGERINTLVRYLLHRAKKGIMRRADVSMAN--FFSCISTLCIGAAAFSH 172
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 134 TMLLTAASQRLSL--LTHVPLSLWSMKMGMDPRRA--ACNRLVALGLGVYVTCFL 186
QY 173 IGAAPFSHYEHWFEOAYYCFITLTITGGFDYVALOKDOALOTOPQYVAFSEFYI 228
: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

Db 187 VPATFAHLEAMSEFLDAFYCFISLSTIGLDVYPGE---APGQPYRALYKVLVTYYL 242

Qy 229 LTGLT---VIGAFNLVLRMT-----MNAEDEKR 256

Db 243 FLGLVAMVLVLOTFRHVSDDLHGLTLLPPCPASFNADEDDR 286

RESULT 11

US-09-336-643-81

Sequence 81, Application US/09336643

GENERAL INFORMATION:

APPLICANT: Miller, Andrew P.

APPLICANT: Curran, Mark Edward

APPLICANT: Hu, Ping

APPLICANT: Rutter, Marc

APPLICANT: Wang, Jian-Wang

TITLE OF INVENTION: Novel Human Potassium Channels

FILE REFERENCE: SEQ-15P

CURRENT APPLICATION NUMBER: US/09/336,643

CURRENT FILING DATE: 1999-06-18

PRIOR APPLICATION NUMBER: 60/076,687

PRIOR FILING DATE: 1998-08-07

PRIOR APPLICATION NUMBER: 60/116,448

PRIOR FILING DATE: 1999-01-19

PRIOR APPLICATION NUMBER: PCT/US99/03826

PRIOR FILING DATE: 1999-02-22

NUMBER OF SEQ ID NOS: 87

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 81

LENGTH: 313

TYPE: PR

ORGANISM: H. sapiens

US-09-336-643-81

Query Match 14.5%; Score 295.5; DB 5; Length 313;

Best Local Similarity 31.7%; Pred. No. 3,7e-19;

Matches 90; Conservative 40; Mismatches 95; Indels 59; Gaps 12;

Qy 18 YLVGAANFDLSEPELIERORLELROQLRARN-----LSGGYELE 63

Db 17 YLVGALLVLRLEGHRELRARELETLRAQLQSPCYAARALDAFVERVLAAG---RLG 73

Qy 64 RVLRLKPKHKAQV---RRFAGSEFYATVTTTIGYGAAPSTDGKFCMFEYALLGIP 120

Db 74 RVLVLANAGSANSAPRANDEFSALFEASTLITTYGCTTTLTDGAKFSAIFALLGVP 133

Qy 121 TLVWFOSIGERINTLVRLYLRRAKKGIGM-----RRADVSMAKVVILGFSCISTLC- 172

Db 134 TMLLTASAQRSLTL---LTHVPLSLMSRMGMDEPRRA---ACWHLVALLGVVVTVCF 186

Qy 173 IGAAPFHYEH-WTFEQAUYCYCTTLTTIGFGDYVALOKDQALQTPQ---YVAFSPYI 228

Db 187 VPATFAHLEAMSEFLDAFYCFISLSTIGLDVYPGE---APGQPYRALYKVLVTYYL 242

Qy 229 LTGLT---VIGAFNLVLRMT-----MNAEDEKR 256

Db 243 FLGLVAMVLVLOTFRHVSDDLHGLTLLPPCPASFNADEDDR 286

RESULT 12

US-09-431-367B-5

Sequence 5, Application US/09431367B

GENERAL INFORMATION:

APPLICANT: Curtis, Rory A.J.

TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR

FILE REFERENCE: MNI-074CP

CURRENT APPLICATION NUMBER: US/09/431,367B

CURRENT FILING DATE: 1999-11-01

PRIOR APPLICATION NUMBER: 09/259,951

PRIOR FILING DATE: 1999-03-01

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 5

LENGTH: 332

TYPE: PR

ORGANISM: Homo sapiens

US-09-431-367B-5

Query Match 14.4%; Score 294.5; DB 5; Length 332;

Best Local Similarity 29.9%; Pred. No. 4.9e-15;

Matches 76; Conservative 52; Mismatches 19; Indels 19; Gaps 6;

Qy 8 TLALVCTFTYLVGAANFDLSEPELIERORLELRARV---LSGGYELEERV 66

Db 22 TVLLLTALVLAVALGTFVETLEGRAQDSSRSRORD---MFTCDRLPDLISLRDV 81

Qy 67 LRLKPKHKAQV-----QWRFAGSEFYATVTTTIGYGAAPSTDGKFCMFEYALLGIP 118

Db 82 VQAYKNGASLSNTSMGRMELVGSFFSVSTTTTIGYGAAPSTDGKFCMFEYALLGIP 141

Qy 119 PLTVWFOSIGERINTLVRLYLRRAKKGIGMRADVSMT---LGFSCIS---TLICIG 174

Db 142 PLNLVLRNRLGHLMQGVNHHASR---LGGTMDPDKAKH---LQSGALLSGLLPFLLP 196

Qy 175 AAAPFHYEH-WTFEQAUYCYCTTLTTIGFGDYVALOKDQAL---YVAFSPYIITGLTV 234

Db 197 PLFESHMEGMSYTEGFYAFITLSTVGGDYV-IGMNPSCQ---LWYKMWVSLWILFGMAW 255

Qy 235 IGAFLNLVLRMT 248

Db 256 LALIKILISQLET 269

RESULT 13

US-09-431-367B-11

Sequence 11, Application US/09431367B

GENERAL INFORMATION:

APPLICANT: Curtis, Rory A.J.

TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR

FILE REFERENCE: MNI-074CP

CURRENT APPLICATION NUMBER: US/09/431,367B

CURRENT FILING DATE: 1999-11-01

PRIOR APPLICATION NUMBER: 09/259,951

PRIOR FILING DATE: 1999-03-01

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 11

LENGTH: 401

TYPE: PR

ORGANISM: Homo sapiens

US-09-431-367B-11

Query Match 12.3%; Score 251.5; DB 5; Length 401;

Best Local Similarity 22.9%; Pred. No. 4.7e-15;

Matches 81; Conservative 39; Mismatches 19; Indels 129; Gaps 8;

Qy 9 LALVCTFTYLVGAANFDLSEPELIERORLELRARV---LSGGYELEERV 62

Db 41 LCFICFLVTVLAVGAVVSALIEDGOVLAADDEFEKEL---RLKNGSEYVEDEKODL 100

Qy 63 ERVVLRLKPKH---KAGVQWRFAGSEFYATVTTTIGYGAAPSTDGKFCMFEYALLGIP 120

Db 101 OGHLQKVKAPQWENRTTHMSLSLFECCVSTVGVGY---FLRGYLCMLYALFGIPL 160

Qy 121 TLVWFOSIGERINTLVRLYLRRAKKGIGM-----RRADVSMAKVVILGFSCISTLC- 172

Db 161 MFLVLTDTGDLATLITSTYNRFRKFPFTPLRLSKWCP---KKKPKPADAVPOIT 220

Qy 146 ----- 145

Db 221 ISAEPLPKLCTGCSRSCEMELFERSHALEKONTLOI---AMRSNSCEPLVIGRLSY 280

Qy 146 -----GLQMRADVSMAKVVIL---GFSCISTLC---AAFSHYE-HWTFEQAUYCYC 193

```
DB 281 SIISNDEVOQOVERLIDIPITALIVFAYISC-----AAAILPEWETOLDPENAFYFC 334
OY 194 FITLTITIGFDGYVALQDQALQTOPOVYAFSVYILGLVIGAFNLVYLRFM 247
DB 335 FVILITIGFDIVL-----EHPNFELEFSYITIVGMEIVFAFKLVONRLI 380
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Search completed: August 28, 2001, 17:11:45  
Job time: 389 sec

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RESULT 14
US-09-746-491-63
; Sequence 63, Application US/09746491
; GENERAL INFORMATION:
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-621
; CURRENT APPLICATION NUMBER: US/09/746,491
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: USSN 60/171,329
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-746-491-63
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Query Match 8.8%; Score 179; DB 5; Length 39;
Best Local Similarity 87.2%; Pred. No. 8.9e-10;
Matches 34; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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OY 338 TCVEQSHSPGGGGRYSDTPSRRLCSGAPRSAISSYST 376
DB 1 TCVEHSHSPGGGGRYSDTPSRRLCSGTRSAISSYST 39
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RESULT 15
US-09-760-469-1386
; Sequence 1386, Application US/09760469
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT254
; CURRENT APPLICATION NUMBER: US/09/760,469
; CURRENT FILING DATE: 2001-01-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1983
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1386
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-760-469-1386
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Query Match 6.6%; Score 135.5; DB 5; Length 205;
Best Local Similarity 34.4%; Pred. No. 6e-05;
Matches 43; Conservative 17; Mismatches 48; Indels 17; Gaps 5;
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OY 148 GMRADVSMANVLIIGFSCISTLCIGAAAFSHYE-HMFPQAYVYCFITLTITIGFDYV 206
DB 42 GFESKQYVAIVHAYLVGVTVSCFFPIPAVAFVLEDDWNFLSFYCFISLSTIGLDYV 101
OY 207 A-----LQKDALQTOPOVYAFSVYILTG---LTVIGAFNLVVL---RFTMNADEK 255
DB 102 PGEGYQKQFEREL-----YKIGITCYLLGLIAMLVLETFCEHLKFRKMFYVKKDKD 156
OY 256 RDAEH 260
DB 157 EDQVH 161
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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 28, 2001, 17:11:13 ; Search time 242.67 Seconds  
(without alignments)  
375.734 Million cell updates/sec

Title:

US-09-503-089A-4

Perfect score:

2090  
1 MAADPLDLPKSAQNSKPRL.....LNGTTPHCAGEDIATVEMNK 411

Sequence:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2803329 seqs, 221847457 residues

Total number of hits satisfying chosen parameters: 2803329

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

Pending\_Patents\_AA\_Main:\*

1: /cgn2\_6/ptodata/2/paa/PCTUS\_COMB.pep:\*  
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5: /cgn2\_6/ptodata/2/paa/US081\_COMB.pep:\*  
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10: /cgn2\_6/ptodata/2/paa/US086\_COMB.pep:\*  
11: /cgn2\_6/ptodata/2/paa/US087\_COMB.pep:\*  
12: /cgn2\_6/ptodata/2/paa/US088\_COMB.pep:\*  
13: /cgn2\_6/ptodata/2/paa/US089\_COMB.pep:\*  
14: /cgn2\_6/ptodata/2/paa/US090\_COMB.pep:\*  
15: /cgn2\_6/ptodata/2/paa/US091\_COMB.pep:\*  
16: /cgn2\_6/ptodata/2/paa/US092\_COMB.pep:\*  
17: /cgn2\_6/ptodata/2/paa/US093\_COMB.pep:\*  
18: /cgn2\_6/ptodata/2/paa/US094\_COMB.pep:\*  
19: /cgn2\_6/ptodata/2/paa/US095\_COMB.pep:\*  
20: /cgn2\_6/ptodata/2/paa/US096\_COMB.pep:\*  
21: /cgn2\_6/ptodata/2/paa/US097\_COMB.pep:\*  
22: /cgn2\_6/ptodata/2/paa/US098\_COMB.pep:\*  
23: /cgn2\_6/ptodata/2/paa/US099\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2090	100.0	411	19	US-09-503-089A-4
2	2084	99.7	411	22	US-09-828-746-6
3	2044	97.8	411	1	PCT-US99-03826-83
4	2044	97.8	411	17	US-09-336-643-83
5	2044	97.8	411	17	US-09-336-643-83
6	2044	97.7	411	22	US-09-828-746-2
7	2041	97.7	411	19	US-09-503-089A-2
8	2011	96.2	426	12	US-08-816-011-45
9	2011	96.2	426	12	US-08-816-011-45
10	2011	96.2	426	12	US-08-816-011C-45

	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	
	1864	1855	1855	1251.5	1251.5	1250	1207.5	1224	797	797	797	797	797	797	797	797	770.5	753.5	753.5	752	640.5	551	510	506	420	420	420	420	420	420	420	420	420	420	420	420
	89.2	88.8	88.8	59.9	59.9	59.8	57.8	58.6	38.1	38.1	38.1	38.1	38.1	38.1	38.1	36.9	36.1	36.1	36.0	30.6	26.4	24.4	24.2	20.1	20.1	20.1	20.1	20.1	20.1	20.1	20.1	20.1	20.1	20.1	20.1	
	370	370	370	543	543	543	484	484	392	392	392	392	392	392	392	392	1779	1785	1785	1616	1068	107	295	110	499	499	499	499	499	499	499	499	499	499	499	
	US-09-655-272-4	US-09-144-914-8	US-09-436-265-8	PCT-US01-14965-7	US-09-852-386-7	US-60-207-583-3	US-60-216-547-1	US-60-230-445-16	PCT-US00-349838-55	US-09-729-739-55	US-09-432-470-2	US-09-432-470-4	US-09-828-035-2	US-60-258-275-4	PCT-US00-349838-55	US-09-729-739-55	US-09-655-272-2	US-60-212-358-1	US-60-207-416-9	US-60-229-525-3	US-60-212-358-1	US-09-828-746-4	US-60-223-269-8	US-60-171-487-5	US-09-259-951-2	US-09-259-951-4	US-09-357-425-1	US-09-436-265-2	US-09-561-763-2	US-09-735-169-2	US-09-735-169-4	US-09-735-169-4	US-09-735-169-4	US-09-735-171-2	US-09-735-171-4	US-09-735-171A
	Sequence 4, Appl	Sequence 8, Appl	Sequence 8, Appl	Sequence 73, Appl	Sequence 376, App	Sequence 10, Appl	Sequence 1632, Ap	Sequence 55, Appl	Sequence 2, Appl	Sequence 2, Appl	Sequence 2, Appl	Sequence 2, Appl	Sequence 2, Appl	Sequence 2, Appl	Sequence 2, Appl	Sequence 2, Appl	Sequence 2, Appl	Sequence 2, Appl	Sequence 2, Appl	Sequence 2, Appl	Sequence 2, Appl	Sequence 2, Appl	Sequence 2, Appl	Sequence 2, Appl	Sequence 2, Appl	Sequence 2, Appl	Sequence 2, Appl	Sequence 2, Appl	Sequence 2, Appl	Sequence 2, Appl	Sequence 2, Appl	Sequence 2, Appl	Sequence 2, Appl	Sequence 2, Appl	Sequence 2, Appl	

#### ALIGNMENTS

RESULT 1  
US-09-503-089A-4  
Sequence 4, Application US/09503089A  
GENERAL INFORMATION:  
APPLICANT: PATEL, AMANDA J.  
APPLICANT: HONORE, ERIC  
APPLICANT: LESAGE, FLORIAN  
APPLICANT: ROMERY, GEORGES  
APPLICANT: LAZDUSKI, MICHEL  
TITLE OF INVENTION: A method for the identification of anesthetics  
FILE REFERENCE: f17b12pro3-humanagTRK  
CURRENT APPLICATION NUMBER: US/09/503,089A  
CURRENT FILING DATE: 2000-02-11  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: Microsoft Word 2000  
SEQ ID NO 4  
LENGTH: 411  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-503-089A-4

Query Match 100.0%; Score 2090; DB 19; Length 411;  
Best Local Similarity 100.0%; Pred. No. 5; Indels 0; Gaps 0;  
Matches 411; Conservative 0; Mismatches 0

QY 1 MAADPLDLPKSAQNSKPRLSFSSKPTVLASRVSDSAF.....AKTVSTIFLVVLYLI 60  
DB 1 MAADPLDLPKSAQNSKPRLSFSSKPTVLASRVSDSAF.....AKTVSTIFLVVLYLI 60  
QY 61 GAAVFALEPOEISORTTIVIKOTFTIAQACVNSTELML100IYVAINAGIIPLGNS 120  
DB 61 GAAVFALEPOEISORTTIVIKOTFTIAQACVNSTELML100IYVAINAGIIPLGNS 120

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QY 121 SNOVSHMDLSSFFPAGYITTTGFCNISPRTGKIFCIYALLGIPLEGFLAGVGDQ 180
    |||||||
Db 121 SNOVSHMDLSSFFPAGYITTTGFCNISPRTGKIFCIYALLGIPLEGFLAGVGDQ 180
QY 181 LGTIFGKGIKAVEDPFIKNNVSQTKIRIISTITIFLFGCVLPALPAVIFKHIEGMSALD 240
    |||||||
Db 181 LGTIFGKGIKAVEDPFIKNNVSQTKIRIISTITIFLFGCVLPALPAVIFKHIEGMSALD 240
QY 241 AITFVVITLTITGFDYVAGSDIEYLDYKPYVWFMILVGLAFYAAVLSMIGDMLRVIS 300
    |||||||
Db 241 AITFVVITLTITGFDYVAGSDIEYLDYKPYVWFMILVGLAFYAAVLSMIGDMLRVIS 300
QY 301 KKTKEEVGEFRAHAAMWTANVTAEFEKTRRLSVEIYDKFORATSVKRLSAELAGNHQ 360
    |||||||
Db 301 KKTKEEVGEFRAHAAMWTANVTAEFEKTRRLSVEIYDKFORATSVKRLSAELAGNHQ 360
QY 361 ELTPCRRITLSVNHLTISEREVLPLLKAESITYLNGLTPHCAGEDIAVIENMK 411
    |||||||
Db 361 ELTPCRRITLSVNHLTISEREVLPLLKAESITYLNGLTPHCAGEDIAVIENMK 411

```

## RESULT 2

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US-09-828-746-6
; Sequence 6, Application US/09828746
; GENERAL INFORMATION:
; APPLICANT: Helen Jane Meadows
; APPLICANT: Conrad Gerald Chapman
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30031-DI
; CURRENT APPLICATION NUMBER: US/09/828,746
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: US 09/236,080
; PRIOR FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: EP 98300570.3
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: UK 9822135.1
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 411
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-828-746-6

```

Abv

Pre grant Pub.

20020028485

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Query Match 99.7%; Score 2084; DB 22; Length 411;
Best Local Similarity 99.8%; Pred. No. 2.1e-203;
Matches 410; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MAAPDLDPKSAONSKPRLSPFSKPTVLASRVESDAINVMKKTGSTIFLVVLYLII 60
    |||||||
Db 1 MAAPDLDPKSAONSKPRLSPFSKPTVLASRVESDAINVMKKTGSTIFLVVLYLII 60
QY 61 GAAVFKALBPQEIISORTIIVIOKOTFIAOHACVNSTEDELIOQIVAAINAGIIPLGNS 120
    |||||||
Db 61 GAAVFKALBPQEIISORTIIVIOKOTFIAOHACVNSTEDELIOQIVAAINAGIIPLGNS 120
QY 121 SNOVSHMDLSSFFPAGYITTTGFCNISPRTGKIFCIYALLGIPLEGFLAGVGDQ 180
    |||||||
Db 121 SNOVSHMDLSSFFPAGYITTTGFCNISPRTGKIFCIYALLGIPLEGFLAGVGDQ 180
QY 181 LGTIFGKGIKAVEDPFIKNNVSQTKIRIISTITIFLFGCVLPALPAVIFKHIEGMSALD 240
    |||||||
Db 181 LGTIFGKGIKAVEDPFIKNNVSQTKIRIISTITIFLFGCVLPALPAVIFKHIEGMSALD 240
QY 241 AITFVVITLTITGFDYVAGSDIEYLDYKPYVWFMILVGLAFYAAVLSMIGDMLRVIS 300
    |||||||
Db 241 AITFVVITLTITGFDYVAGSDIEYLDYKPYVWFMILVGLAFYAAVLSMIGDMLRVIS 300
QY 301 KKTKEEVGEFRAHAAMWTANVTAEFEKTRRLSVEIYDKFORATSVKRLSAELAGNHQ 360
    |||||||
Db 301 KKTKEEVGEFRAHAAMWTANVTAEFEKTRRLSVEIYDKFORATSVKRLSAELAGNHQ 360

```

```

Db 301 KKTKEEVGEFRAHAAMWTANVTAEFEKTRRLSVEIYDKFORATSVKRLSAELAGNHQ 360
    |||||||
QY 361 ELTPCRRITLSVNHLTISEREVLPLLKAESITYLNGLTPHCAGEDIAVIENMK 411
    |||||||
Db 361 ELTPCRRITLSVNHLTISEREVLPLLKAESITYLNGLTPHCAGEDIAVIENMK 411

```

## RESULT 3

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PCT-US99-03826-83
; Sequence 83, Application PC/TUS9903826A
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew
; APPLICANT: Curran, Mark
; TITLE OF INVENTION: NOVEL Human Potassium Channel
; FILE REFERENCE: SEQ-15PCT
; CURRENT APPLICATION NUMBER: PCT/US99/03826A
; CURRENT FILING DATE: 1999-02-22
; EARLIER APPLICATION NUMBER: 60/076,687
; EARLIER FILING DATE: 1998-02-25
; EARLIER APPLICATION NUMBER: 60/095,836
; EARLIER FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: 60/116,448
; EARLIER FILING DATE: 1999-01-19
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 83
; LENGTH: 411
; TYPE: PRT
; ORGANISM: H. sapiens
PCT-US99-03826-83

```

```

Query Match 97.8%; Score 2044; DB 1; Length 411;
Best Local Similarity 96.4%; Pred. No. 2.6e-19;
Matches 396; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

```

```

QY 1 MAAPDLDPKSAONSKPRLSPFSKPTVLASRVESDAINVMKKTGSTIFLVVLYLII 60
    |||||||
Db 1 MAAPDLDPKSAONSKPRLSPFSKPTVLASRVESDAINVMKKTGSTIFLVVLYLII 60
QY 61 GAAVFKALBPQEIISORTIIVIOKOTFIAOHACVNSTEDELIOQIVAAINAGIIPLGNS 120
    |||||||
Db 61 GAAVFKALBPQEIISORTIIVIOKOTFIAOHACVNSTEDELIOQIVAAINAGIIPLGNS 120
QY 121 SNOVSHMDLSSFFPAGYITTTGFCNISPRTGKIFCIYALLGIPLEGFLAGVGDQ 180
    |||||||
Db 121 SNOVSHMDLSSFFPAGYITTTGFCNISPRTGKIFCIYALLGIPLEGFLAGVGDQ 180
QY 181 LGTIFGKGIKAVEDPFIKNNVSQTKIRIISTITIFLFGCVLPALPAVIFKHIEGMSALD 240
    |||||||
Db 181 LGTIFGKGIKAVEDPFIKNNVSQTKIRIISTITIFLFGCVLPALPAVIFKHIEGMSALD 240
QY 241 AITFVVITLTITGFDYVAGSDIEYLDYKPYVWFMILVGLAFYAAVLSMIGDMLRVIS 300
    |||||||
Db 241 AITFVVITLTITGFDYVAGSDIEYLDYKPYVWFMILVGLAFYAAVLSMIGDMLRVIS 300
QY 301 KKTKEEVGEFRAHAAMWTANVTAEFEKTRRLSVEIYDKFORATSVKRLSAELAGNHQ 360
    |||||||
Db 301 KKTKEEVGEFRAHAAMWTANVTAEFEKTRRLSVEIYDKFORATSVKRLSAELAGNHQ 360
QY 361 ELTPCRRITLSVNHLTISEREVLPLLKAESITYLNGLTPHCAGEDIAVIENMK 411
    |||||||
Db 361 ELTPCRRITLSVNHLTISEREVLPLLKAESITYLNGLTPHCAGEDIAVIENMK 411

```

## RESULT 4

```

US-09-336-643-83
; Sequence 83, Application US/09336643
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew
; APPLICANT: Curran, Mark
; APPLICANT: Ping Hu
; APPLICANT: Marc Rutler

```

6,399,761



```

; APPLICANT: Jian-Ying Wang
; TITLE OF INVENTION: Novel Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/09/336,643
; EARLIER FILING DATE: 1999-06-18
; EARLIER APPLICATION NUMBER: 60/095,836
; EARLIER FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: 60/116,448
; EARLIER FILING DATE: 1999-01-19
; EARLIER APPLICATION NUMBER: PCT/US99/03826
; EARLIER FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 83
; LENGTH: 411
; TYPE: PRT
; ORGANISM: H. sapiens
US-09-336-643-83

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Query Match          97.8%; Score 2044; DB 17; Length 411;
Best Local Similarity 96.4%; Pred. No. 2.6e-199;
Matches 396; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

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QY 1 MAAPDLDPKSAONSKPRLSFSKPTVLASRVESDSAIVMKKTVSTFLVVLII 60
    |||||||
DB 1 MAAPDLDPKSAONSKPRLSFSKPTVLASRVESDPTINMKKTVSTFLVVLII 60
    |||||||
QY 61 GAUFKALKEOPHEISQRTTVIOKQFIHQACVNSTEDELIOQIYAALNAGIIPGNS 120
    |||||||
DB 61 GAUFKALKEOPHEISQRTTVIOKQFIHQACVNSTEDELIOQIYAALNAGIIPGNT 120
    |||||||
QY 121 SNOVSHMDLSSFFAGTIVTTIGFNGISPRTEGKIFCIITALLGIPLEGFLAGVDQ 180
    |||||||
DB 121 SNOVSHMDLSSFFAGTIVTTIGFNGISPRTEGKIFCIITALLGIPLEGFLAGVDQ 180
    |||||||
QY 181 LGTIFGKIAKVEDTFIKMNVSOQTKIRIISTIIIFLFGCVLPAVPAVIFKHIEGMSALD 240
    |||||||
DB 181 LGTIFGKIAKVEDTFIKMNVSOQTKIRIISTIIIFLFGCVLPAVPAVIFKHIEGMSALD 240
    |||||||
QY 241 AIFVVTITLTIGFGDVAGSDIEYIDFKRPVWFWILGLAVFAVLSMIGDMLRVIS 300
    |||||||
DB 241 AIFVVTITLTIGFGDVAGSDIEYIDFKRPVWFWILGLAVFAVLSMIGDMLRVIS 300
    |||||||
QY 301 KKTKEVEGEFRANAEHTANVTAEFKETRRRLSVEIYDKFORATSVKRLSAELAGNHQ 360
    |||||||
DB 301 KKTKEVEGEFRANAEHTANVTAEFKETRRRLSVEIYDKFORATSVKRLSAELAGNHQ 360
    |||||||
QY 361 ELTPCRRTLISVNHLSERDVLPLPLKTESIYINGLTPHCAGEELAVIENIK 411
    |||||||
DB 361 ELTPCRRTLISVNHLSERDVLPLPLKTESIYINGLTPHCAGEELAVIENIK 411
    |||||||

```

```

RESULT 5
US-09-336-643-83
; Sequence 83, Application US/09336643A
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rutler, Marc
; TITLE OF INVENTION: Novel Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/09/336,643A
; EARLIER FILING DATE: 1999-06-18
; EARLIER APPLICATION NUMBER: 60/076,687
; EARLIER FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: 60/116,448
; EARLIER FILING DATE: 1999-01-19
; EARLIER APPLICATION NUMBER: PCT/US99/03826
; EARLIER FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 411
; TYPE: PRT
; ORGANISM: H. sapiens
US-09-336-643-83

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Query Match          97.8%; Score 2044; DB 17; Length 411;
Best Local Similarity 96.4%; Pred. No. 2.6e-199;
Matches 396; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

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QY 1 MAAPDLDPKSAONSKPRLSFSKPTVLASRVESDSAIVMKKTVSTFLVVLII 60
    |||||||
DB 1 MAAPDLDPKSAONSKPRLSFSKPTVLASRVESDPTINMKKTVSTFLVVLII 60
    |||||||
QY 61 GAUFKALKEOPHEISQRTTVIOKQFIHQACVNSTEDELIOQIYAALNAGIIPGNS 120
    |||||||
DB 61 GAUFKALKEOPHEISQRTTVIOKQFIHQACVNSTEDELIOQIYAALNAGIIPGNT 120
    |||||||
QY 121 SNOVSHMDLSSFFAGTIVTTIGFNGISPRTEGKIFCIITALLGIPLEGFLAGVDQ 180
    |||||||
DB 121 SNOVSHMDLSSFFAGTIVTTIGFNGISPRTEGKIFCIITALLGIPLEGFLAGVDQ 180
    |||||||
QY 181 LGTIFGKIAKVEDTFIKMNVSOQTKIRIISTIIIFLFGCVLPAVPAVIFKHIEGMSALD 240
    |||||||
DB 181 LGTIFGKIAKVEDTFIKMNVSOQTKIRIISTIIIFLFGCVLPAVPAVIFKHIEGMSALD 240
    |||||||
QY 241 AIFVVTITLTIGFGDVAGSDIEYIDFKRPVWFWILGLAVFAVLSMIGDMLRVIS 300
    |||||||
DB 241 AIFVVTITLTIGFGDVAGSDIEYIDFKRPVWFWILGLAVFAVLSMIGDMLRVIS 300
    |||||||
QY 301 KKTKEVEGEFRANAEHTANVTAEFKETRRRLSVEIYDKFORATSVKRLSAELAGNHQ 360
    |||||||
DB 301 KKTKEVEGEFRANAEHTANVTAEFKETRRRLSVEIYDKFORATSVKRLSAELAGNHQ 360
    |||||||
QY 361 ELTPCRRTLISVNHLSERDVLPLPLKTESIYINGLTPHCAGEELAVIENIK 411
    |||||||
DB 361 ELTPCRRTLISVNHLSERDVLPLPLKTESIYINGLTPHCAGEELAVIENIK 411
    |||||||

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RESULT 6
US-09-828-746-2
; Sequence 2, Application US/09828746
; GENERAL INFORMATION:
; APPLICANT: Helen Jane Meadows
; APPLICANT: Conrad Gerald Chapman
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30031-D1
; CURRENT APPLICATION NUMBER: US/09/828,746
; EARLIER FILING DATE: 2001-04-09
; EARLIER APPLICATION NUMBER: US/09/236,080
; EARLIER FILING DATE: 1999-01-25
; EARLIER APPLICATION NUMBER: EP 98300570.3
; EARLIER FILING DATE: 1998-01-27
; EARLIER APPLICATION NUMBER: UK 9822135.1
; EARLIER FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 411
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-828-746-2

```

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Query Match          97.8%; Score 2044; DB 17; Length 411;
Best Local Similarity 96.4%; Pred. No. 2.6e-199;
Matches 396; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

```

```

QY 1 MAAPDLDPKSAONSKPRLSFSKPTVLASRVESDSAIVMKKTVSTFLVVLII 60
    |||||||
DB 1 MAAPDLDPKSAONSKPRLSFSKPTVLASRVESDPTINMKKTVSTFLVVLII 60
    |||||||

```

26020.28485  
ABN

QY 61 GAAVEKALBOPHISORTTIVIOKOTFIQAHOACVNSTELDELIOQIVAAINAGIPLGNS 120  
 DB 61 GAAVEKALBOPHISORTTIVIOKOTFIQAHOACVNSTELDELIOQIVAAINAGIPLGNT 120  
 QY 121 SNOVSHMDLGSFFAGVITTTIGFNGNISPRTEGKIFCIIYALLGIPLEGFLLAGVGDO 180  
 DB 121 SNOVSHMDLGSFFAGVITTTIGFNGNISPRTEGKIFCIIYALLGIPLEGFLLAGVGDO 180  
 QY 181 LGTIFEGKIAKVEDTFIKNNVSOTKIRIISTITIFLFGCVLPAALPAVIFKHIEGMSALD 240  
 DB 181 LGTIFEGKIAKVEDTFIKNNVSOTKIRIISTITIFLFGCVLPAALPAVIFKHIEGMSALD 240  
 QY 241 AITFVVITTTIGFGDYVAGSGDIEYLDYKPYVWFMILVGLAFYAVLSMIGDMLRVIS 300  
 DB 241 AITFVVITTTIGFGDYVAGSGDIEYLDYKPYVWFMILVGLAFYAVLSMIGDMLRVIS 300  
 QY 301 KKTKEVGEFRAHAEMWTANVTAEFEKTRRLSVEIYDKFORATSVKRLSLAELAGNHQ 360  
 DB 301 KKTKEVGEFRAHAEMWTANVTAEFEKTRRLSVEIYDKFORATSVKRLSLAELAGNHQ 360  
 QY 361 ELTPCRRLTSVNHLSEREVLPLKASITYLNGLTPHAGEDIAYIENMK 411  
 DB 361 ELTPCRRLTSVNHLSEREVLPLKASITYLNGLTPHAGEDIAYIENMK 411

## RESULT 7

US-09-503-089a-2  
 ; Sequence 2, Application US/09503089A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: PATEL, AMANDA J.  
 ; APPLICANT: HONORE, ERIC  
 ; APPLICANT: LESAGE, FLORIAN  
 ; APPLICANT: ROMNEY, GEORGES  
 ; APPLICANT: LAZDUSKI, MICHEL  
 ; TITLE OF INVENTION: A method for the identification of anesthetics  
 ; FILE REFERENCE: f17b12prov3-humantrek  
 ; CURRENT APPLICATION NUMBER: US/09/503,089A  
 ; NUMBER OF SEQ ID NOS: 5  
 ; SOFTWARE: Microsoft Word 2000  
 ; SEQ ID NO 2  
 ; LENGTH: 411  
 ; TYPE: PRF  
 ; ORGANISM: Homo sapiens  
 US-09-503-089a-2

*not out*

Query Match 97.7%; Score 2041; DB 19; Length 411;  
 Best Local Similarity 96.1%; Pred. No. 5, 2e-199;  
 Matches 395; Conservative 12; Mismatches 4; Indels 0; Gaps 0;

QY 1 MAAPDLDPKSAONSKPRLSFSSKPTVLASRVESDAINVMKVTSTFLVLYLII 60  
 DB 1 MAAPDLDPKSAONSKPRLSFSSKPTVLASRVESDTTINVMKVTSTFLVLYLII 60  
 QY 61 GAAVEKALBOPHISORTTIVIOKOTFIQAHOACVNSTELDELIOQIVAAINAGIPLGNS 120  
 DB 61 GAAVEKALBOPHISORTTIVIOKOTFIQAHOACVNSTELDELIOQIVAAINAGIPLGNT 120  
 QY 121 SNOVSHMDLGSFFAGVITTTIGFNGNISPRTEGKIFCIIYALLGIPLEGFLLAGVGDO 180  
 DB 121 SNOVSHMDLGSFFAGVITTTIGFNGNISPRTEGKIFCIIYALLGIPLEGFLLAGVGDO 180  
 QY 181 LGTIFEGKIAKVEDTFIKNNVSOTKIRIISTITIFLFGCVLPAALPAVIFKHIEGMSALD 240  
 DB 181 LGTIFEGKIAKVEDTFIKNNVSOTKIRIISTITIFLFGCVLPAALPAVIFKHIEGMSALD 240  
 QY 241 AITFVVITTTIGFGDYVAGSGDIEYLDYKPYVWFMILVGLAFYAVLSMIGDMLRVIS 300  
 DB 241 AITFVVITTTIGFGDYVAGSGDIEYLDYKPYVWFMILVGLAFYAVLSMIGDMLRVIS 300  
 QY 301 KKTKEVGEFRAHAEMWTANVTAEFEKTRRLSVEIYDKFORATSVKRLSLAELAGNHQ 360  
 DB 301 KKTKEVGEFRAHAEMWTANVTAEFEKTRRLSVEIYDKFORATSVKRLSLAELAGNHQ 360

DB 301 KKTKEVGEFRAHAEMWTANVTAEFEKTRRLSVEIYDKFORATSVKRLSLAELAGNHQ 360  
 QY 361 ELTPCRRLTSVNHLSEREVLPLKASITYLNGLTPHAGEDIAYIENMK 411  
 DB 361 ELTPCRRLTSVNHLSEREVLPLKASITYLNGLTPHAGEDIAYIENMK 411

## RESULT 8

US-08-816-011-45  
 ; Sequence 45, Application US/08816011  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Price, Laura A.  
 ; APPLICANT: Pausch, Mark H.  
 ; TITLE OF INVENTION: Potassium Channels, Nucleotide Sequences  
 ; TITLE OF INVENTION: Encoding Them, and Methods of Using Same  
 ; NUMBER OF SEQUENCES: 56  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: American Home Products Corporation  
 ; STREET: One Campus Drive  
 ; CITY: Parsippany  
 ; STATE: New Jersey  
 ; COUNTRY: USA  
 ; ZIP: 07054  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/816,011  
 ; FILING DATE: 11-MAR-1997  
 ; CLASSIFICATION: 536  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Matthews, Gale F.  
 ; REGISTRATION NUMBER: 32,269  
 ; REFERENCE/DOCKET NUMBER: 32,421-C2  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 201-683-2134  
 ; TELEFAX: 201-683-4117  
 ; INFORMATION FOR SEQ ID NO: 45:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 426 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 US-08-816-011-45

3/11/97

20030165806

Query Match 96.2%; Score 2011; DB 12; Length 426;  
 Best Local Similarity 95.1%; Pred. No. 6, 3e-176;  
 Matches 391; Conservative 13; Mismatches 4; Indels 0; Gaps 0;

QY 1 MAAPDLDPKSAONSKPRLSFSSKPTVLASRVESDAINVMKVTSTFLVLYLII 60  
 DB 16 VAAPDLDPKSAONSKPRLSFSSKPTVLASRVESDTTINVMKVTSTFLVLYLII 75  
 QY 61 GAAVEKALBOPHISORTTIVIOKOTFIQAHOACVNSTELDELIOQIVAAINAGIPLGNS 120  
 DB 76 GAAVEKALBOPHISORTTIVIOKOTFIQAHOACVNSTELDELIOQIVAAINAGIPLGNT 135  
 QY 121 SNOVSHMDLGSFFAGVITTTIGFNGNISPRTEGKIFCIIYALLGIPLEGFLLAGVGDO 180  
 DB 136 SNOVSHMDLGSFFAGVITTTIGFNGNISPRTEGKIFCIIYALLGIPLEGFLLAGVGDO 195  
 QY 181 LGTIFEGKIAKVEDTFIKNNVSOTKIRIISTITIFLFGCVLPAALPAVIFKHIEGMSALD 240  
 DB 196 LGTIFEGKIAKVEDTFIKNNVSOTKIRIISTITIFLFGCVLPAALPAVIFKHIEGMSALD 255  
 QY 241 AITFVVITTTIGFGDYVAGSGDIEYLDYKPYVWFMILVGLAFYAVLSMIGDMLRVIS 300  
 DB 256 AITFVVITTTIGFGDYVAGSGDIEYLDYKPYVWFMILVGLAFYAVLSMIGDMLRVIS 315

OY 301 KKTKEEVEGFRAHAAEWNTANTAEKTRRLRLSEIYDKFORATSVKRRKLSAELAGNHQ 360  
DB 316 KKTKEEVEGFRAHAAEWNTANTAEKTRRLRLSEIYDKFORATSVKRRKLSAELAGNHQ 375  
OY 361 ELTPCRRLTSVNHLSREVDLPPLKKAESIYLNGLTPHAGEDJAVIENMK 411  
DB 376 ELTPCRRLTSVNHLSREVDLPPLKKAESIYLNGLTPHAGEDJAVIENMK 426

RESULT 9

US-08-816-011A-45  
Sequence 45, Application US/08816011A  
GENERAL INFORMATION:  
APPLICANT: Pausch, Laura A.  
APPLICANT: Pausch, Mark H.  
TITLE OF INVENTION: Potassium Channels, Nucleotide Sequences  
TITLE OF INVENTION: Encoding Them, and Methods of Using Same  
NUMBER OF SEQUENCES: 56  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: American Home Products Corporation  
STREET: One Campus Drive  
CITY: Parsippany  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07054  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/816,011A  
FILING DATE: 11-MAR-1997  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Matthews, Gale F.  
REGISTRATION NUMBER: 32,269  
REFERENCE/DOCKET NUMBER: 32,421-C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-683-2134  
TELEFAX: 201-683-4117  
INFORMATION FOR SEQ ID NO: 45:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 426 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-816-011A-45

Query Match 96.2% Score 2011; DB 12; Length 426;  
Best Local Similarity 95.1% Pred. No. 6.3e-196;  
Matches 391; Conservative 13; Mismatches 7; Indels 0; Gaps 0;

OY 1 MAAPDLDPKSAQNSKPRLSFSKPTVLASRVESDSAINVMKKTSTIFLVVLYLI 60  
DB 16 VAAPDLDPKSAQNSKPRLSFSKPTVLASRVESDPTINVMKKTSTIFLVVLYLI 75  
OY 61 GAAVFKALEQPOEISORTTIVIOKOTFLAHCYNSDELDELIOQIVAAINAGIIPLGNS 120  
DB 76 GATVFKALEQPOEISORTTIVIOKOTFLAHCYNSDELDELIOQIVAAINAGIIPLGNT 135  
OY 121 SNOVSHMDLSSFFACTVITTTIGFGNISPRTEGKIFCIITIALGIPLEFLLAGVGDQ 180  
DB 136 SNOVSHMDLSSFFACTVITTTIGFGNISPRTEGKIFCIITIALGIPLEFLLAGVGDQ 195  
OY 181 LGTFGKIAKVEDTFTKMNVSQTKIRIISTIFILFGCVLFVALPAVIFKHIGMSALD 240  
DB 196 LGTFGKIAKVEDTFTKMNVSQTKIRIISTIFILFGCVLFVALPAVIFKHIGMSALD 255  
OY 241 AIYFVVITLTTIGFGDVVAGSDIEYLDYKPPVWFMLVGLAFAVLSMIGMLRVIS 300  
DB 256 AIYFVVITLTTIGFGDVVAGSDIEYLDYKPPVWFMLVGLAFAVLSMIGMLRVIS 315

OY 301 KKTKEEVEGFRAHAAEWNTANTAEKTRRLRLSEIYDKFORATSVKRRKLSAELAGNHQ 360  
DB 316 KKTKEEVEGFRAHAAEWNTANTAEKTRRLRLSEIYDKFORATSVKRRKLSAELAGNHQ 375  
OY 361 ELTPCRRLTSVNHLSREVDLPPLKKAESIYLNGLTPHAGEDJAVIENMK 411  
DB 376 ELTPCRRLTSVNHLSREVDLPPLKKAESIYLNGLTPHAGEDJAVIENMK 426

RESULT 10

US-08-816-011C-45  
Sequence 45, Application US/08816011C  
GENERAL INFORMATION:  
APPLICANT: Pausch, Mark H.  
APPLICANT: Pausch, Laura A.  
TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,  
FILE REFERENCE: 01142.0122 SEQUENCE LISTING  
CURRENT FILING DATE: 1997-03-11  
PRIORITY FILING DATE: 08/332, 312  
PRIOR FILING DATE: 1994-10-31  
PRIOR APPLICATION NUMBER: PCT/US95/14364  
PRIOR FILING DATE: 1995-10-25  
NUMBER OF SEQ ID NOS: 64  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 45  
LENGTH: 426  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-08-816-011C-45

Query Match 96.2% Score 2011; DB 12; Length 426;  
Best Local Similarity 95.1% Pred. No. 6.3e-196;  
Matches 391; Conservative 13; Mismatches 7; Indels 0; Gaps 0;

OY 1 MAAPDLDPKSAQNSKPRLSFSKPTVLASRVESDSAINVMKKTSTIFLVVLYLI 60  
DB 16 VAAPDLDPKSAQNSKPRLSFSKPTVLASRVESDPTINVMKKTSTIFLVVLYLI 75  
OY 61 GAAVFKALEQPOEISORTTIVIOKOTFLAHCYNSDELDELIOQIVAAINAGIIPLGNS 120  
DB 76 GATVFKALEQPOEISORTTIVIOKOTFLAHCYNSDELDELIOQIVAAINAGIIPLGNT 135  
OY 121 SNOVSHMDLSSFFACTVITTTIGFGNISPRTEGKIFCIITIALGIPLEFLLAGVGDQ 180  
DB 136 SNOVSHMDLSSFFACTVITTTIGFGNISPRTEGKIFCIITIALGIPLEFLLAGVGDQ 195  
OY 181 LGTFGKIAKVEDTFTKMNVSQTKIRIISTIFILFGCVLFVALPAVIFKHIGMSALD 240  
DB 196 LGTFGKIAKVEDTFTKMNVSQTKIRIISTIFILFGCVLFVALPAVIFKHIGMSALD 255  
OY 241 AIYFVVITLTTIGFGDVVAGSDIEYLDYKPPVWFMLVGLAFAVLSMIGMLRVIS 300  
DB 256 AIYFVVITLTTIGFGDVVAGSDIEYLDYKPPVWFMLVGLAFAVLSMIGMLRVIS 315  
OY 301 KKTKEEVEGFRAHAAEWNTANTAEKTRRLRLSEIYDKFORATSVKRRKLSAELAGNHQ 360  
DB 316 KKTKEEVEGFRAHAAEWNTANTAEKTRRLRLSEIYDKFORATSVKRRKLSAELAGNHQ 375  
OY 361 ELTPCRRLTSVNHLSREVDLPPLKKAESIYLNGLTPHAGEDJAVIENMK 411  
DB 376 ELTPCRRLTSVNHLSREVDLPPLKKAESIYLNGLTPHAGEDJAVIENMK 426

RESULT 11  
US-09-655-272-4  
Sequence 4, Application US/09655272  
GENERAL INFORMATION:  
APPLICANT: HONORE, ERIC  
APPLICANT: FINK, MICHEL

```

; APPLICANT: LAZDUNSKI, MICHEL
; APPLICANT: LESAGE, FLORIAN
; APPLICANT: DUPRAT, FABRICE
; TITLE OF INVENTION: MECHANOSENSITIVE MAMMALIAN POTASSIUM CHANNELS
; TITLE OF INVENTION: ACTIVATABLE BY POLYUNSATURATED FATTY ACIDS AND THE USE
; TITLE OF INVENTION: OF SAID CHANNELS IN DRUG SCREENING
; FILE REFERENCE: 1383-00
; CURRENT APPLICATION NUMBER: US/09/655,272
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: PCT/FR99/00404
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: FR 98/02725
; PRIOR FILING DATE: 1998-03-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 4
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Unknown Sequence
; FEATURE:
; OTHER INFORMATION: Description of Unknown Sequence: TREK
US-09-655-272-4

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Query Match      89.2%; Score 1864; DB 20; Length 370;
Best Local Similarity 99.7%; Pred. No. 5.3e-181;
Matches 367; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 1 MAAPDLDPKSAQNSKPRLSFSKPTVLASRVESDAINVMKTVSTIFLVVLYLII 60
DB 1 MAAPDLDPKSAQNSKPRLSFSKPTVLASRVESDAINVMKTVSTIFLVVLYLII 60
OY 61 GAAVFALBPOEISORTTIVIOKOTFFIAOHACVNSTEDELIOQIVAAINAGIIPLGNS 120
DB 61 GAAVFALBPOEISORTTIVIOKOTFFIAOHACVNSTEDELIOQIVAAINAGIIPLGNS 120
OY 121 SNQVSHMDLSSFFAGVYITTTGFGNISPRTEGKIFCTIYALGIPLEGFLAGVGQD 180
DB 121 SNQVSHMDLSSFFAGVYITTTGFGNISPRTEGKIFCTIYALGIPLEGFLAGVGQD 180
OY 181 LGTIFGKIAKVEDPFIKNNVSQTKIRIISTIFILFGCVLVALPAVIFKHIIEGSALD 240
DB 181 LGTIFGKIAKVEDPFIKNNVSQTKIRIISTIFILFGCVLVALPAVIFKHIIEGSALD 240
OY 241 AIYFVYITTTGFGDYVAGSDIEYLDYKPYVWFMIILGLVFAAVLSMIGDMLRVIS 300
DB 241 AIYFVYITTTGFGDYVAGSDIEYLDYKPYVWFMIILGLVFAAVLSMIGDMLRVIS 300
OY 301 KTKKEVGEFRAHAEMTANVTAEFKETRRLSVEIYDKFORATSVKRLSAELAGNHNO 360
DB 301 KTKKEVGEFRAHAEMTANVTAEFKETRRLSVEIYDKFORATSVKRLSAELAGNHNO 360
OY 361 ELTPCRRRT 368
DB 361 ELTPCRRRT 368

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RESULT 12
US-09-144-914-8
; Sequence 8, Application US/09144914
; GENERAL INFORMATION:
; APPLICANT: Duprat, Fabrice
; APPLICANT: Lesage, Florian
; APPLICANT: Fink, Michel
; APPLICANT: Lazdunski, Michel
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
; TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
; FILE REFERENCE: 989,6705CIP
; CURRENT APPLICATION NUMBER: US/09/144,914
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 08/749,816
; EARLIER FILING DATE: 1996-11-15
; EARLIER APPLICATION NUMBER: 60/095,234

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; EARLIER FILING DATE: 1998-08-04
; EARLIER APPLICATION NUMBER: FR 96/01565
; EARLIER FILING DATE: 1996-02-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 8
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Murine
; FEATURE:
; OTHER INFORMATION: TREK-1
US-09-144-914-8

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Query Match      88.8%; Score 1855; DB 20; Length 370;
Best Local Similarity 99.5%; Pred. No. 4.4e-177;
Matches 366; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 1 MAAPDLDPKSAQNSKPRLSFSKPTVLASRVESDAINVMKTVSTIFLVVLYLII 60
DB 1 MAAPDLDPKSAQNSKPRLSFSKPTVLASRVESDAINVMKTVSTIFLVVLYLII 60
OY 61 GAAVFALBPOEISORTTIVIOKOTFFIAOHACVNSTEDELIOQIVAAINAGIIPLGNS 120
DB 61 GAAVFALBPOEISORTTIVIOKOTFFIAOHACVNSTEDELIOQIVAAINAGIIPLGNS 120
OY 121 SNQVSHMDLSSFFAGVYITTTGFGNISPRTEGKIFCTIYALGIPLEGFLAGVGQD 180
DB 121 SNQVSHMDLSSFFAGVYITTTGFGNISPRTEGKIFCTIYALGIPLEGFLAGVGQD 180
OY 181 LGTIFGKIAKVEDPFIKNNVSQTKIRIISTIFILFGCVLVALPAVIFKHIIEGSALD 240
DB 181 LGTIFGKIAKVEDPFIKNNVSQTKIRIISTIFILFGCVLVALPAVIFKHIIEGSALD 240
OY 241 AIYFVYITTTGFGDYVAGSDIEYLDYKPYVWFMIILGLVFAAVLSMIGDMLRVIS 300
DB 241 AIYFVYITTTGFGDYVAGSDIEYLDYKPYVWFMIILGLVFAAVLSMIGDMLRVIS 300
OY 301 KTKKEVGEFRAHAEMTANVTAEFKETRRLSVEIYDKFORATSVKRLSAELAGNHNO 360
DB 301 KTKKEVGEFRAHAEMTANVTAEFKETRRLSVEIYDKFORATSVKRLSAELAGNHNO 360
OY 361 ELTPCRRRT 368
DB 361 ELTPCRRRT 368

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RESULT 13
US-09-436-265-8
; Sequence 8, Application US/09436265
; GENERAL INFORMATION:
; APPLICANT: REYES, ROBERTO
; APPLICANT: DUPRAT, FABRICE
; APPLICANT: LESAGE, FLORIAN
; APPLICANT: FINK, MICHEL
; APPLICANT: SALINAS, MIGUEL
; APPLICANT: FARMAN, NICOLETTE
; APPLICANT: LAZDUNSKI, MICHEL
; TITLE OF INVENTION: NEW FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR
; TITLE OF INVENTION: CLONING AND THEIR USE, ESPECIALLY FOR THE SCREENING OF
; TITLE OF INVENTION: DRUGS
; FILE REFERENCE: 1201-CIP2-00
; CURRENT APPLICATION NUMBER: US/09/436,265
; CURRENT FILING DATE: 1999-11-08
; PRIOR APPLICATION NUMBER: 60/095,234
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/107,692
; PRIOR FILING DATE: 1996-11-09
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 8
; LENGTH: 370
; TYPE: PRT

```

ORGANISM: Murine sp.  
FEATURE:  
OTHER INFORMATION: TREK-1  
US-09-436-265-8

Query Match 88.8%; Score 1855; DB 18; Length 370;  
Best Local Similarity 99.5%; Pred. No. 4,4e-180;  
Matches 366; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 1 MAADLLDPKSAONSKPRLSFSSKPTPLASRVSDSAINMKKTSTIFLVVLYLI 60  
D 1 MAADLLDPKSAONSKPRLSFSSKPTPLASRVSDSAINMKKTSTIFLVVLYLI 60  
Y 61 GAAVFAKLEQPOEISORTTIVIOKOTFIAHACYNSTELDELIOQIYVAI 120  
D 61 GAAVFAKLEQPOEISORTTIVIOKOTFIAHACYNSTELDELIOQIYVAI 120  
Y 121 SNOVSHMDLGSFFPACTVITTTGPGNISPTREGKIFCIIYALLGIP 180  
D 121 SNOVSHMDLGSFFPACTVITTTGPGNISPTREGKIFCIIYALLGIP 180  
Y 181 LGTFEGKIAVEDPTFKMNSOTKIRIISTIFILFCVLFVALPNIHIGMSLD 240  
D 181 LGTFEGKIAVEDPTFKMNSOTKIRIISTIFILFCVLFVALPNIHIGMSLD 240  
Y 241 AIYFVITLTTIGFGDYVAGSDIEYDFYKPVWFMILGLAFPAVLSMIGMLRYS 300  
D 241 AIYFVITLTTIGFGDYVAGSDIEYDFYKPVWFMILGLAFPAVLSMIGMLRYS 300  
Y 301 KTIKEVGEFRAHAEMTANTVTAFFKTRRLSVEIYDKFORATSVKRKLSAELAGNHQ 360  
D 301 KTIKEVGEFRAHAEMTANTVTAFFKTRRLSVEIYDKFORATSVKRKLSAELAGNHQ 360  
Y 361 ELTPCRRT 368  
D 361 ELTPCRRT 368

RESULT 14  
PCT-US01-14965-73  
Sequence 73, Application PC/TUS0114965  
GENERAL INFORMATION:  
APPLICANT: Pharmacia & Upjohn Company  
APPLICANT: Roberts, Steven L.  
APPLICANT: Benjamin, Christopher  
APPLICANT: Karnovsky, Alla M.  
APPLICANT: Ruble, Cara L.  
TITLE OF INVENTION: Human Ion Channels  
FILE REFERENCE: 00133.PCT1  
CURRENT APPLICATION NUMBER: PCT/US01/14965  
CURRENT FILING DATE: 2001-05-10  
PRIOR APPLICATION NUMBER: 60/203,305  
PRIOR FILING DATE: 2000-05-10  
PRIOR APPLICATION NUMBER: 60/207,092  
PRIOR FILING DATE: 2000-05-25  
PRIOR APPLICATION NUMBER: 60/206,526  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,033  
PRIOR FILING DATE: 2000-05-25  
PRIOR APPLICATION NUMBER: 60/207,093  
PRIOR FILING DATE: 2000-05-25  
PRIOR APPLICATION NUMBER: 60/216,893  
PRIOR FILING DATE: 2000-07-17  
PRIOR APPLICATION NUMBER: 60/237,873  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: 60/223,245  
PRIOR FILING DATE: 2000-08-04  
NUMBER OF SEQ ID NOS: 88  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 73  
LENGTH: 543  
TYPE: PRT

ORGANISM: Homo sapiens  
PCT-US01-14965-73

Query Match 59.9%; Score 1251.5; DB 1; Length 543;  
Best Local Similarity 64.3%; Pred. No. 3,4e-110;  
Matches 247; Conservative 54; Mismatches 46; Indels 17; Gaps 5;

Y 2 AADLLDPKSA-----AONSKPRLSFSSKPTPLASRVSDS--AINMKKTSTI 50  
D 22 AAAYCQPKSKTNOQPPAPATPTPRLSISRATYVA-K-UTSOGGLQYMKKTIVAI 80  
Y 51 FLVVVLLIIGAFAKLEQPOEISORTTIVIOKOTFIAHACYNSTELDELIOQIYVAI 110  
D 81 FVVVVVLLVGTGLVFALEQPFESSOKNTALEKAEFL-HVCSYPOELTLEIHALDAD 140  
Y 111 NAGIIFPLGNSNOVSHMDLGSFFPACTVITTTGPGNISPTREGKIFCIIYALLGIP 170  
D 141 NAGVSPIGNSSNNSHMDLGSFAFFPACTVITTTGPGNISPTREGKIFCIIYALLGIP 200  
Y 171 GFLLAGVGDQGTTFEGKIAVEDPTFKMNSOTKIRIISTIFILFCVLFVALPNIHIGMSLD 230  
D 201 GFLLAGVGDQGTTFEGKIAVEDPTFKMNSOTKIRIISTIFILFCVLFVALPNIHIGMSLD 260  
Y 231 KHIGMSALDAIYFVITLTTIGFGDYVAGG-SDIEYDFYKPVWFMILGLAFPAVLSMIGMLRYS 289  
D 261 KYIEGWTFLESITFVYVITLTTIGFGDYVAGGSDIEYDFYKPVWFMILGLAFPAVLSMIGMLRYS 320  
Y 290 SMIGMLRYSKTIKEVGEFRAHAEMTANTVTAFFKTRRLSVEIYDKFORATSV--- 346  
D 321 SMIGMLRYSKTIKEVGEFRAHAEMTANTVTAFFKTRRLSVEIYDKFORATSV--- 380  
Y 347 -KRKLSAELAGNHQDELTPCRRTL 369  
D 381 ERRRLGDQRAHSLDMLSPKRSV 404

RESULT 15  
US-09-852-386-73  
Sequence 73, Application US/09852386  
GENERAL INFORMATION:  
APPLICANT: Roberts, Steven L.  
APPLICANT: Benjamin, Christopher  
APPLICANT: Karnovsky, Alla M.  
APPLICANT: Ruble, Cara L.  
TITLE OF INVENTION: Human Ion Channels  
FILE REFERENCE: 00133.US1  
CURRENT APPLICATION NUMBER: US/09/852,386  
CURRENT FILING DATE: 2001-05-10  
PRIOR APPLICATION NUMBER: 60/203,305  
PRIOR FILING DATE: 2000-05-10  
PRIOR APPLICATION NUMBER: 60/207,092  
PRIOR FILING DATE: 2000-05-25  
PRIOR APPLICATION NUMBER: 60/206,526  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,033  
PRIOR FILING DATE: 2000-05-25  
PRIOR APPLICATION NUMBER: 60/207,093  
PRIOR FILING DATE: 2000-05-25  
PRIOR APPLICATION NUMBER: 60/216,893  
PRIOR FILING DATE: 2000-07-17  
PRIOR APPLICATION NUMBER: 60/237,873  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: 60/223,245  
PRIOR FILING DATE: 2000-08-04  
NUMBER OF SEQ ID NOS: 88  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 73  
LENGTH: 543  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-852-386-73





Db 241 AIVFVITLTITIGFDYVAGSGDIEYLDYFKPVVFWMLVGLAFVAVLSMIGDWLRVIS 300  
 QY 301 KKTKEVEGERAAAEWTAANTVAEFKTRRLSVEIYDKFORATSIKRLSAELAGNHQ 360  
 Db 301 KKTKEVEGERAAAEWTAANTVAEFKTRRLSVEIYDKFORATSIKRLSAELAGNHQ 360  
 QY 361 ELTPCRRRLSVNHLTNERDVLPPDLKTESIYINGLTPHCAGEEIAVENIK 411  
 Db 361 ELTPCRRRLSVNHLTNERDVLPPDLKTESIYINGLTPHCAGEEIAVENIK 411

# RESULT 2

US-09-431-367B-2  
 ; Sequence 2, Application US/09431367B  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Curtis, Roy A.J.  
 ; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR  
 ; FILE REFERENCE: MNI-074CP  
 ; CURRENT APPLICATION NUMBER: US/09/431,367B  
 ; CURRENT FILING DATE: 1999-11-01  
 ; PRIOR APPLICATION NUMBER: 09/259,951  
 ; PRIOR FILING DATE: 1999-03-01  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SOFTWARE: Patentln Ver. 2.0  
 ; SEQ ID NO 2  
 ; LENGTH: 499  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-431-367B-2

## Query Match

20.3%; Score 427; DB 5; Length 499;  
 Best Local Similarity 31.1%; Pred. No. 2,9e-31;  
 Matches 106; Conservative 60; Mismatches 121; Indels 54; Gaps 11;

QY 54 VLYLIIGATVFKALDOPHEISQRTTIVIQKOTFISQHSQVNSTELDELIOQIVAAIMAG 113  
 Db 12 IIFYLAIGAAIFEVLEBPHKRAKNVYQKHLKEFCLGEGDLKILEVSDAAGG 71  
 QY 114 IILGNTSNISHWDLGSSFFAGVITTTIGFNGNISPRTEGKRIFFCIYALGIPLEGFL 173  
 Db 72 VAITGNOT--FNMMNPMNAIFATVITTTIGVNAKPPAGHLFCVFGVPL--C 126  
 QY 174 LAGVGDLGTIFGKGIKAKVDFEIKMVSOTKIRIISTIFILFGCVLFEVALPAIFKH 233  
 Db 127 LHWI-SALGKFFGKRAKRLGQFLTKGVSLSRKQITCTVFIYMGVYLHLVITPPVMT 185  
 QY 234 EGSWALDAIVFVITLTITIGFDYVAG-GSDIEYLDYFKPVVFWMLVGLAFVAVLSMT 292  
 Db 186 EGMNYIEGLYFSTITISTIGFDVAGVNSANYHALRYFVELMVIYGLAM---LSLF 241  
 QY 293 GDMLRVSKTKKEVEGERAAAEWTAANTVAEFKTRRLSVEIYDKFORATSIKRLSA 352  
 Db 242 VNM-----KVSF-----VEVHKAIKRRRR-----KRESF 267  
 QY 353 ELAGNHQELTPCRRRLSVNHLTNERDV--LPPLKTESIY 391  
 Db 268 E-SSPHS-----RKALOVAGSTASKDVNIFLSKKEEY 301

## RESULT 3

US-09-431-367B-5  
 ; Sequence 5, Application US/09431367B  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Curtis, Roy A.J.  
 ; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR  
 ; FILE REFERENCE: MNI-074CP  
 ; CURRENT APPLICATION NUMBER: US/09/431,367B  
 ; CURRENT FILING DATE: 1999-11-01  
 ; PRIOR APPLICATION NUMBER: 09/259,951  
 ; PRIOR FILING DATE: 1999-03-01  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SOFTWARE: Patentln Ver. 2.0

; SEQ ID NO 5  
 ; LENGTH: 332  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-431-367B-5

## Query Match

18.6%; Score 391; DB 4; Length 332;  
 Best Local Similarity 35.9%; Pred. No. 3.2e-11;  
 Matches 89; Conservative 51; Mismatches 31; Indels 14; Gaps 6;

QY 50 IFLVVLYLIIGATVFKALDOPHEISQRTTIVIQKOTFISQHSQVNSTELDELIOQIVAA 109  
 Db 25 LILAYLALYALGTGVFWTELEGRAODSSRSFORDKWEILLFCIDRPALDLSIRDVQA 84  
 QY 110 INAGIIPGNTSNISHWDLGSSFFAGVITTTIGFNGNISPRTEGKRIFFCIYALGIP 169  
 Db 85 YKNGASLSNTTS-MGRWELVGSFFSVSTITIGYGNLS--TMAARLFCIFALVGIPL 143  
 QY 170 FGLAGVGDOLGTIFGKGI---AKVEDFTKMNVSQRTTIVIQKOTFISQHSQVNSTELDELIOQIVAA 225  
 Db 144 NLVVL-----NRLGHLMOQGVNHRASRLGCT---NQ-DPKK--NLASGALLSGLLFL 195  
 QY 226 PAIFKHIEGWSALDAIVFVITLTITIGFDYVAGSGDIE-YLDYFKPVVFWMLVGLAF 284  
 Db 196 PLLFSGHMEGWSYTEGFPYAFITLSTVGFDYVIGMNPQSRPYLVYKNNYSILILEGMAM 255  
 QY 285 FAVLSMT 292  
 Db 256 LALILKLI 263

## RESULT 4

US-09-798-584-15  
 ; Sequence 15, Application US/09798584  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mu, David  
 ; APPLICANT: Powers, Scott  
 ; APPLICANT: Tularik Inc.  
 ; TITLE OF INVENTION: KCNB: A Novel Potassium Channel Protein  
 ; FILE REFERENCE: 018/81-00401005  
 ; CURRENT APPLICATION NUMBER: US/09/798,584  
 ; CURRENT FILING DATE: 2001-03-03  
 ; PRIOR APPLICATION NUMBER: US 60/186,951  
 ; PRIOR FILING DATE: 2000-03-03  
 ; NUMBER OF SEQ ID NOS: 18  
 ; SOFTWARE: Patentln Ver. 2.1  
 ; SEQ ID NO 15  
 ; LENGTH: 394  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; OTHER INFORMATION: human potassium channel K<sub>1</sub> (TASK1)  
 US-09-798-584-15

QY 42 MKWVSTIFLVV--VLYLIIGATVFKALDOPHEISQRTTIVIQKOTFISQHSQVNS--T 97  
 Db 1 MKRQVRLTALIVCTPTVLYGNAVFDALSEBELIERO--LRQELBARVLSGGYE 60  
 QY 98 ELDELIOQIVAAIMAGIIPGNTSNISHWDLGSSFFAGVITTTIGFNGNISPRTEGKRI 157  
 Db 61 ELERVVRL-KPHKAGV-----QMRFASEYFVITTTIGYHAAPSTDGGRV 108  
 QY 158 FCIYALGIPLEGFLAGDOLGTIF-----GRKAKVEDFTKMNVSQTKIRI 208  
 Db 109 FCMFYALGIPLTVMFQSTIGERINTLVRLHRAKGI--RRAD-----VSM 156  
 QY 209 ISTIIFLEGCVLVALPAIFKHIEGWSALDAIVFVITLTITIGFDYVAGSGD--IEY 266

## Query Match

17.3%; Score 363; DB 4; Length 394;  
 Best Local Similarity 31.0%; Pred. No. 1.5e-11;  
 Matches 91; Conservative 59; Mismatches 31; Indels 42; Gaps 9;



```

; LENGTH: 374
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human KCNB (Potassium Channel) expressed in Breast)
US-09-798-584-1

```

```

RESULT 5
US-09-746-491-60
; Sequence 60, Application US/09746491
; GENERAL INFORMATION:
; APPLICANT: Burgess, Catherine E.
; FILE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-621
; CURRENT APPLICATION NUMBER: US/09/746,491
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: USSN 60/171,329
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.0
; LENGTH: 365
; SEQ ID NO 60
; TYPE: PRT
; ORGANISM: Cavia porcellus
US-09-746-491-60

```

```

Query Match
Best Local Similarity 17.0%; Score 357.5; DB 5; Length 365;
Matches 94; Conservative 60; Mismatches 109; Indels 49; Gaps 9;

```

```

QY 42 MKMKTSTFLV--VLYLIIGATVEKALDOPHEISORTTIVIOKOTFISQHSVCNSTEL 99
DB 1 MKRONVATLSLICTFTYLLVGAADFALSDHMEEREKKAKEIRIKGYNT--STED 58
QY 100 DELIQIVAA--NAGIIPLGNTSNOISHMDLSSFFPAGVITTTGGFNGISPTREGK 156
DB 59 YRQLELVIILOSEPHRAGV-----QMKFAGSFYFALTITTTGGYGAAGCTDAGK 107
QY 157 IFCTIYALGIPLEFGFLAGVGDOGTIFGKIAKVEDTPIK-----NVSQTKIR 207
DB 108 AFCEFAVADLIPILVMEQSLGERM-----NTEVRALKRIKCCGMNTEVS 155
QY 208 IISTIIILFGCVLPAIIFKHIKIEGMSALDAIVFVITLTIGFDVYAGSD--IE 265
DB 156 MENVVTVGFSCMGTLCIGAASFQCEBMSFHAHYCCFTITTTIGFDVYALOSKALQ 215
QY 266 YLDFKPVVFWILVGLAFPAVLMSIGDMLRVISKTKKEEVEGFAHAA-----EWTA 319
DB 216 RKPFYVAFSFWIIVGLVIGAFILNV--VLRFITMNSDEBGEGBGALPGNPSVVT 273
QY 320 NVTAPEKETRRL 331
DB 274 HISEARQVROR 285

```

```

RESULT 6
US-09-798-584-1
; Sequence 1, Application US/09798584
; GENERAL INFORMATION:
; APPLICANT: Mu, David
; APPLICANT: Powers, Scott
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: KCNB: A Novel Potassium Channel Protein
; FILE REFERENCE: 018781-004010US
; CURRENT APPLICATION NUMBER: US/09/798,584
; PRIOR FILING DATE: 2001-03-03
; PRIOR APPLICATION NUMBER: US 60/186,951
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1

```

```

; LENGTH: 374
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human KCNB (Potassium Channel) expressed in Breast)
US-09-798-584-1

```

```

Query Match
Best Local Similarity 16.6%; Score 349.5; DB 5; Length 374;
Matches 106; Conservative 77; Mismatches 116; Indels 63; Gaps 12;

```

```

QY 42 MKMKTSTFLV--VLYLIIGATVEKALDOPHEISORTTIVIOKOTFISQHSVCNSTEL 99
DB 1 MKRONVATLSLICTFTYLLVGAADFALSDHMEEREKKAKEIRIKGYNT--STED 58
QY 100 DELIQIVAA--NAGIIPLGNTSNOISHMDLSSFFPAGVITTTGGFNGISPTREGK 157
DB 60 RQLELVIILOSEPHRAGV-----QMKFAGSFYFALTITTTGGYGAAGCTDAGK 108
QY 158 FCTIYALGIPLEFGFLAGVGDOGTIFGKIAKVEDTPIK-----NVSQTKIRI 208
DB 109 FCMFYAVLGIPLVMEQSLGERM-----NTEVRALKRIKCCGMNTEVS 156
QY 209 IISTIIILFGCVLPAIIFKHIKIEGMSALDAIVFVITLTIGFDVYAGSD--IE 265
DB 157 ENMTVGVGFSCMGTLCIGAASFQCEBMSFHAHYCCFTITTTIGFDVYALOSKALQ 216
QY 267 LDFKPVVFWILVGLAFPAVLMSIGDMLRVISKTKK--VEGFAHAA-----EWTA 320
DB 217 KPLVAFSFWIIVGLVIGAFILNV--VLRFITMNSDEBGEGBGALPGNPSVVT 274
QY 321 VTAEFKETRRLSVEI-----YDKFORATSKRLSALAGNHNDELPCR 366
DB 275 IPEEPRSRPRKADVDLDQSCVCTCRSDYCGREVA--MNSATLAPHYFHSISKYI 334
QY 367 RTLSVNHILNERDVLPLLTETISYILNGLTPH 398
DB 335 EISPSILKN--SLFSPISISPLGHSFTDH 364

```

```

RESULT 7
US-09-431-367B-8
; Sequence 8, Application US/09431367B
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNT-074CB
; CURRENT APPLICATION NUMBER: US/09/431,367B
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: 09/259,951
; PRIOR FILING DATE: 1999-03-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-431-367B-8

```

```

Query Match
Best Local Similarity 16.6%; Score 348; DB 5; Length 313;
Matches 83; Conservative 42; Mismatches 104; Indels 12; Gaps 5;

```

[illegible]

```

RESULT      8
US-09-336-643-81
: Sequence 81, Application US/09336643
: GENERAL INFORMATION:
: APPLICANT: Miller, Andrew P.
: APPLICANT: Curran, Mark Edward
: APPLICANT: Hu, Ping
: APPLICANT: Rutler, Marc
: APPLICANT: Wang, Jian-Wang
: TITLE OF INVENTION: Novel Human Potassium Channels
: FILE REFERENCE: SEQ-15
: CURRENT APPLICATION NUMBER: US/09/336,643
: CURRENT FILING DATE: 1999-06-18
: PRIOR APPLICATION NUMBER: 60/076,687
: PRIOR FILING DATE: 1998-08-07
: PRIOR APPLICATION NUMBER: 60/116,448
: PRIOR FILING DATE: 1999-01-19
: PRIOR APPLICATION NUMBER: PCT/US99/03826
: PRIOR FILING DATE: 1999-02-22
: NUMBER OF SEQ ID NOS: 87
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 81
: LENGTH: 313
: TYPE: PRT
: ORGANISM: H. saplens
US-09-336-643-81

```

Query Match	16.6%	Score 348	DB 58	Length 313
Best Local Similarity	34.4%	Pred. No. 2,6e-24		
Matches	83	Conservative	42	Mismatches 104, Indels 12, Gaps 5
QY	57	YIIGATYFKALQEPHEISQRTTIIYIQKOTFISQHCNVSTELDELLIQOIVAINAGIIP	116	
		:	:	:
Db	17	LYVLIALIVARLEGHEARLRALELTFLRAQLLRQSRCAVAPALDAVEREVLAAAGRGRRV	76	
QY	117	LQNTSNOIS---HMDLGSPFAGVITITIGFNGSPTEGGKICITIIYALGIDPLFG	172	
		:	:	:
Db	77	LAMAGSNAASDPAMDPAFASLITITVGYGTYTLPETLDAGKATASIFALLGVFTMI	136	
QY	173	LLAGVGDDLGITFGGCIKAVEDETFIKMANSQIRIISITITIFLFGCVLFAV--LPAIIF	230	
		:	:	:
Db	137	LTTASAQRIISL---LTHVPLSMISMRGMDPRRAACMHLVALLGVVTVCEPLVAEVI	192	
QY	231	KHI-EGMSALDAIYFVVIILTTIGEGDYAAGSDIE-YLDFYKPVVWFMLIVAFVAV	288	
		:	:	:
Db	193	AHLEAMSLDAFYFCFISLSTIGIGDGVYGGAEAPQGRPYATKVKLVITVYLLFLGLVAMVLI	252	
QY	289	L 289		
Db	253	L 253		

```

RESULT      9
US-09-746-491-59
: Sequence 59, Application US/09746491
: GENERAL INFORMATION
: APPLICANT: Burgess, Catherine E.
: TITLE OR INVENTION: Novel Proteins and Nucleic Acids Encoding Same
: FILE REFERENCE: 15966-621

```

```

:
: CURRENT APPLICATION NUMBER: US/09/746,491
:
: CURRENT FILING DATE: 2000-12-20
:
: PRIOR APPLICATION NUMBER: USSN 60/171,329
:
: PRIOR FILING DATE: 1999-12-21
:
: NUMBER OF SEQ ID NOS: 72
:
: SOFTWARE: PatentIn Ver. 2.0
:
: SEQ ID NO 59
:
:   LENGTH: 330
:   TYPE: prt
:
: ORGANISM: Homo sapiens
:
: US-09-746-491-59

```

	Query Match	16.5%	Score 347.5:	13 :	Length 330;
	Best Local Similarity	34.9%:	Pred. No. 3,1e-24:		
	Matches	91,	Conservative	42:	Mismatches 95; Indels 33; Gaps
Oy	50	IFLVVYLIIIGATVFKALEDPHEISORTTIVIOKQFISO--HSCVNSTELDELIOOI	106		
Db	11	LVLCTICLLGAAVFDALDESEAE-SGROILLYOKRALRKPFQFSADRYEIERLALO-	68		
Oy	107	VAAIAGIITPIGNMNSQIASHMDLSSPEFFACTVTTTGT-N-SPTSGKIFCIYALLG	166		
Db	69	AEPHRAG-----RQKKPFGSFEFALTVTITTC "HAMPGTOSGKVCFCMFYALLG	117		
Oy	167	IPLPEGLLAGVDOLGITTEGGIAKVEDTF-IKNWVSOFKIT-IISTIIPIILFGCVLFVAL	225		
Db	118	IPLTLVPFQSIGERINNAVRRLLLAAKCCLGRMTCASTE---NLNVAGILMACAATIAL	173		
Oy	226	PAIEFKIHIEGSALDAIFVVYITLTITIGFGDYVGCSGD IEYIDFYKRPVNF--WIITVL	282		
Db	174	GAVAFSHREGMTFPFAHYVYCITILTITIGFGDFVALQSG-AIQKRLPYVAFSFLYITLGL	232		
Oy	283	AYFAAVLSMI-----GDW 295			
Db	233	TVIGAFLNVLVLRFLVASADM 233			

```

RESULT 10
US-09-746-491-61
: Sequence 61. Application US/09746491
: GENERAL INFORMATION:
: APPLICANT: Burgess, Catherine E.
: TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
: FILE REFERENCE: 15966-621
: CURRENT APPLICATION NUMBER: US/09/746,491
: PRIOR FILING DATE: 2000-12-20
: PRIOR APPLICATION NUMBER: USSN 60/171,329
: NUMBER OF SEQ ID NOS: 72
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 61
: LENGTH: 258
: TYPE: PRT
: ORGANISM: Mus musculus
US-09-746-491-61

```

	Query Match Similarity	16.3%	Score 342.5;	DB 5:	Length 258;	
	Best Local Similarity	30.0%	Pred. No. 6.3e-24;			
	Matches	84;	Conservative	61;	Mismatches	94;
					Indels	41;
					Gaps	8
OY	42	MKMKTVSTFLVV--VLVLIIGATVFKALEQHEISQRTTYIVOKOTFISHCSVNS--T	97			
		:   :   :    :	:          :	: : :	:	:
Db	1	MKRQWVRITLALVCGFTYLTVGAAVFDALESEPEMERIKELRQLRLARNLSSGEVE	60			
OY	98	EIDELLIOQTVAIINNGIIPLGNTSMOISHWDJASSFEFGAVITYTGICNISPREEGKI	157			
		: : : :    :	:             :	: :    :	:	:
Db	61	ELERVVLRL-KPKHAGV-----QMRFAGSGEYFAIVITTYIGYGHAPSTGGGV	108			
OY	158	PCIIYAALGIPLRGFLLAGVGSDGLTIFFCKGLAKNYEDTLKNNVSQTK-----IKI	208			
		:             :	:	:	:	:
Db	109	FCMFALLGIPLTLTWFSQSLGERI-----NTEVRLLRHAKGLGMRAAEVVM	156			

```

? RESULT 12
? US-09-746-491-22
? Sequence 22, Application US/09746491
? GENERAL INFORMATION:
? APPLICANT: Burgess, Catherine E.
? TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
? FILE REFERENCE: 15966-621
? CURRENT APPLICATION NUMBER: US/09/746,491
? CURRENT FILING DATE: 2000-12-20
? PRIOR APPLICATION NUMBER: USSN 60/171,329
? PRIOR FILING DATE: 1999-12-21
? NUMBER OF SEQ ID NOS: 72
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 22
? LENGTH: 393
? TYPE: PRT
? ORGANISM: Homo sapiens
? FEATURE:

```

Query Match 9.8%; Score 205; DB 5; Length 401;  
 Best Local Similarity 20.8%; Pred. No. 4.6e-11;  
 Matches 77; Conservative 38; Mismatches 83; Indels 172; Gaps 12.

QY	54	VLLVLIIGATYFKALQEPHEISQRTTIVIQKOTFSQHSVAVSTELDELQOIVAINAG	113
		:     : :	
DB	47	LVTALVAWVFSAIE-----DGVVLA-----DGEFEKLEBLCLRLNCS	89
		:     : :	
QY	114	IIPGNTS-----NOISHWDGSSFEFNA-----TGTGFGNISRTGEGKTF	158
		:     : :	
DB	90	ETVVEDRKQDIDGLHQKAKPQWFMENFTTHSPLSLFPCGCTSYVGCGYITTYTRIGKTL	149
		:     : :	
QY	159	CIYALGCIPLFGELLGAVGDQGTI-----FSGKIAKVVDTFIKW-----	199
		:     : :	
DB	150	CMLYALFEGIPLMFLVLTDTGDILATILSTSYNRFKKFPRFRPLLSKWCPSLFFKKRDP	209
		:     : :	
QY	200	-----	199
DB	210	KPADEAVQIIIIISAELEPGKRLGTCPSPSCSMELFERSHALEKQNTIDLPQAMERSMS	269
		:     : :	
QY	200	-----NVSQT-----KRIISITIIPLHGCVLVAVALPAIIIEKHIEG	235
		:     : :	

```
Db 270 CPELVIGRLSYSTIISNDEVGQOVERLDIPILALIVFAVISCANAI-LPF----- 320
QY 236 W-SALD---AIFVITLTITIGED-----YVAGSDIEY-----L 267
Db 321 WETQLEBNFAYFCVFTLTIGFDVLEHPNPFLEFSPSIYIYGMETVFAFKLVQRLI 380
QY 268 DEFKPVVWF 277
Db 381 DIKNWMLFF 390
```

```
RESULT 14
US-09-336-643-16
; Sequence 16, Application US/09336643
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rulter, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: Novel Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/09/336,643
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 197
; TYPE: PRT
; ORGANISM: H. sapiens
US-09-336-643-16
```

```
Query Match 7.38; Score 153.5; DB 5; Length 197;
Best Local Similarity 27.58; Pred. No. 9e-07;
Matches 52; Conservative 39; Mismatches 65; Indels 33; Gaps 8;
```

```
QY 148 ISPTREGKIFCIITIALGIPLEFLAGVDDIGTFGKIAKVEDTFIKWNVSQTKIR 207
Db 1 MAPLSGKAFCAVYALGIPASIALVATLRHCLLPVLSRPAMVA---VHQLSPARAA 57
QY 208 IISTIFILEGCVLPAIPAIIFKHIEG-WSALDAIYFVITLTITIGFDYVAG-GSDIE 265
Db 58 LLOAVNALGLVASSFVLLPALVLMGLQDCSLGAVYFCFSSISTIGLEDLLPGRGRSLH 117
QY 266 YLDFYKPVWF-----WILGLAVFAFVLSMIGDMLVISKTKKEEYGEFRAHAEM 317
Db 118 -----PVYIHGQLALLGLTLGL-----LAML-----LAVETSELPOVRAMGKFF 159
QY 318 --TANYTAE 324
Db 160 RPSGPVTAE 168
```

```
RESULT 15
US-09-760-469-1386
; Sequence 1386, Application US/09760469
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT254
; CURRENT APPLICATION NUMBER: US/09/760,469
; CURRENT FILING DATE: 2001-01-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1983
; SOFTWARE: PatentIn Ver. 2.0
```

```
; SEQ ID NO 1386
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-760-469-1386
```

```
Query Match 7.18; Score 150; DB 5; Length 205;
Best Local Similarity 30.28; Pred. No. 2e-07;
Matches 39; Conservative 28; Mismatches 50; Indels 12; Gaps 6;
```

```
QY 197 IKWVNSQTKIRIISTII--FILFGCVLFAVLPALPAIFKH1--GWSALDAIYFVITLTITIG 253
Db 39 IRMGFSKQVVAIYHVAVLGFTVWSCFFI--PAAVFSV1--NPFLESFYFCISLSTIG 96
QY 254 FGDYVAG-GSDIEYLDYFKPVVWFMLVGLAYFAVLSMIGDLRVYSK-----KTKEEV 307
Db 97 LGDYVPGEGYNOKFRELYKIGITCYLLGLIAMLVLEFCE-LHELIKFRKMFYVKKDK 155
QY 308 GEFRRAHAE 316
Db 156 DEDQVWHITE 164
```

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Search completed: August 28, 2001, 17:11:44
Job time: 388 sec
```



**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 Comugen Ltd.

OM protein - protein search, using sw model

Run on: August 28, 2001, 17:11:44 ; Search time 24.66 Seconds  
(without alignments)  
357.486 Million cell updates/sec

Title:

US-09-503-089a-4

Perfect score:

2090 1 MAAPDLDPKSAONSKRPL.....LNGLTPHCAGEDIAVIENMK 411

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 154674 seqs, 21449152 residues

Total number of hits satisfying chosen parameters: 154674

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Pending\_Patents\_AA\_New:\*  
1: /cgn2\_6/ptodata/1/paa/PCT\_NEW\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/paa/US06\_NEW\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/paa/US07\_NEW\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/paa/US60\_NEW\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2044	97.8	411	5	US-09-336-643-83
2	420	20.1	499	5	US-09-431-367B-2
3	387	18.5	332	5	US-09-431-367B-5
4	370	17.7	394	5	US-09-798-584-15
5	351.5	16.8	330	5	US-09-746-491-59
6	351.5	16.8	365	5	US-09-746-491-60
7	350.5	16.4	258	5	US-09-746-491-61
8	343.5	16.4	330	5	US-09-746-491-58
9	343.5	16.4	333	5	US-09-746-491-22
10	342.5	16.4	374	5	US-09-798-584-1
11	342	16.4	313	5	US-09-431-367B-8
12	342	16.4	313	5	US-09-336-643-81
13	212	10.1	401	5	US-09-431-367B-11
14	152.5	7.3	197	5	US-09-336-643-16
15	151	7.2	205	5	US-09-760-469-1386
16	128	6.1	988	6	US-60-299-378-2
17	128	6.1	988	6	US-60-300-614-2
18	127	6.1	988	6	US-60-299-378-3
19	127	6.1	988	6	US-60-300-614-3
20	118.5	5.7	989	6	US-60-299-378-6
21	118.5	5.7	989	6	US-60-300-614-6
22	116	5.6	221	6	US-60-299-378-21
23	115	5.6	221	6	US-60-300-614-21
24	115	5.5	962	6	US-60-299-378-4
25	113	5.5	962	6	US-60-300-614-4
26	114	5.5	962	6	US-60-299-378-5
27	114	5.5	962	6	US-60-300-614-5

28	105	5.0	631	6	US-60-299-484-23	Sequence 23, Appl
29	102.5	4.9	273	6	US-60-304-243-6	Sequence 6, Appl1
30	99.5	4.8	254	5	US-09-758-472-7049	Sequence 7029, Ap
31	97.5	4.7	590	5	US-09-803-110-8812	Sequence 8812, Ap
32	96	4.6	355	5	US-09-595-332A-6	Sequence 1905, Ap
33	96	4.6	613	5	US-09-803-110-1340	Sequence 13186, A
34	93.5	4.5	502	5	US-09-803-110-1232	Sequence 12322, A
35	93	4.4	197	5	US-09-738-626-4620	Sequence 4620, Ap
36	93	4.4	468	5	US-09-738-626-4777	Sequence 4777, Ap
37	93	4.4	468	5	US-09-602-787A-612	Sequence 612, App
38	92.5	4.4	460	5	US-09-738-626-6145	Sequence 6145, Ap
39	92.5	4.4	509	5	US-09-573-655A-1266	Sequence 1266, Ap
40	92.5	4.4	538	1	PCT-US01-14827-1210	Sequence 12102, A
41	92.5	4.4	621	1	PCT-US01-14827-1210	Sequence 12101, A
42	92.5	4.4	950	6	US-60-304-243-9	Sequence 9, Appl1
43	91.5	4.4	534	6	US-60-299-484-21	Sequence 21, Appl
44	91.5	4.4	947	6	US-60-304-243-2	Sequence 2, Appl1
45	91.5	4.4	994	6	US-60-304-243-8	Sequence 8, Appl1

#### ALIGNMENTS

```

RESULT 1
US-09-336-643-83
; Sequence 83, Application US/09336643
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rulter, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: Novel Human Potassium Channel
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/09/336,643
; CURRENT FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 411
; TYPE: PRT
; ORGANISM: H. sapiens
US-09-336-643-83

Query Match          97.8% Score 2044; DE: Length 411;
Best Local Similarity 96.4% Pred. No. 6.3e+2
Matches 396; Conservative 11; Mismatches 0; Indels 0; Gaps 0;

1 MAAPDLDPKSAONSKRPLSFSSKPTVLASRVSDSA...KAKKTVSTPLVAVLII 60
|||||
1 MAAPDLDPKSAONSKRPLSFSTKPTVLASRVSDSI...KAKKTVSTPLVAVLII 60
|||||
61 GAAVFALEQPOEISORTTIVIKOTFLAHCAYNSTE...LLIOIVAINAGIIPLGNS 120
|||||
61 GAAVFALEQPOEISORTTIVIKOTFLAHCAYNSTE...LLIOIVAINAGIIPLGNS 120
|||||
61 GATVFALEQPOEISORTTIVIKOTFLAHCAYNSTE...LLIOIVAINAGIIPLGNT 120
|||||
121 SNOVSHMDLGSFFAGVITTTIGFNGISPRTEGKIF...ITVALLGIPFLAGVGDQ 180
|||||
121 SNOVSHMDLGSFFAGVITTTIGFNGISPRTEGKIF...ITVALLGIPFLAGVGDQ 180
|||||
181 LGTFGKIAVEDETFIKMNSOTKIRISITIFLFGCV...VAPVAFHIGGMSLD 240
|||||
181 LGTFGKIAVEDETFIKMNSOTKIRISITIFLFGCV...VAPVAFHIGGMSLD 240
|||||
241 AIVEVITLTTIGFGDVAGSDIEYDFKPVVFWFI...VQAVFAVLSMIGMLRYIS 300
|||||

```

D <b>b</b>	241	AIIEPVITITLTIGRGDGVAGGSDIEIDFKKPVWFMILIVGLAEFAVLISMIDGMLRVIS	300
O <b>y</b>	301	KKTKEEYGEFAAHAAEMTANTYAFKEKTRRLSLSEIYDKFORASTYRKLSAELAGNHQ	360
D <b>b</b>	301	KKTKEEYGEFAAHAAEMTANTYAFKEKTRRLSLSEIYDKFORASTYRKLSAELAGNHQ	360
O <b>y</b>	361	ELTPCRLTSLVNHILTSEREVLPLPLKABSYLNGLTDPHCAGEDIAVTIENKK	411
D <b>b</b>	361	ELTPCRLTSLVNHILTSEREVLPLPLKABSYLNGLTDPHCAGEDIAVTIENKR	411

```

RESULT 2
US-09-431-367B-2
: Sequence 2, Application US/09431367B
: GENERAL INFORMATION:
: APPLICANT: Curtis, Rory A.J
: TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
: FILE REFERENCE: MNI-074CP
: CURRENT APPLICATION NUMBER: US/09/431,367B
: PRIOR FILING DATE: 1999-11-01
: PRIOR APPLICATION NUMBER: 09/259,951
: NUMBER OF SEQ ID NOS: 12
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 2
: LENGTH: 499
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-431-367B-2

```

```

Query Match          20.1%; Score 420; DB 5; Length 459;
Best Local Similarity 30.8%; Pred. No. 4.5e-31;
Matches 105; Conservative 62; Mismatches 120; Indels 54; Gaps 11.

OY 54 VLVYIIIGAAYKALKEOPEOISQRTTIVYIOKQKFTIAOHACVNSTEDELIOOIIVAAINAG 113
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 12 IIFYLAIQRAIEVLEERPEWKKAKKNYYIQKHLHLEKPECLQEOGIDKLIEVVSDAAGG 71
   ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY 114 IIPINSSNOVSHMDLGGSSFFPAGTVITTTIGPNTISPRTEGGKIFCIILYALGIDPLGFL 173
   ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 72 VAITGNQI--FNNMWMPMNMFIAAVITTTIGVGNVAPKPRAGRLFCVFYGLGCVPL--C 126
   ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY 174 IAGVEDQIGTIGKCIAYKVEDFIKMNNSQTKIRIISTIIIFLFGCVLFAVALPAVLFKKI 233
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 127 LTMI-SALGKFFGGRAKRLGQPLFKRGVSLRKAQIQTCTVIFITWGLVHLVYIPPFYMT 185
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY 234 EGMNALDAIEFVYITLTTIGFDGYAAG--GSDIEYIDFEPYVWFWTLVLGVAFAAVLSMI 292
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 166 EEMNNYIEGLIYEFITITISTIGFDPVAGVPSANYHALYIFVELMITYLDLAW---LSLF 241
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY 293 GDMLEIVISKTKKEVEGEFRAHAAEWMTANTVYAEFKETRRRLSVEIYDKFORATSVKRLSLA 352
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 242 VNM-----KVSME-----VEVHKAIKRRRR-----RKSEF 267
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY 353 ELAGNNHQLPCTCRRTLSVNNHLSEREV--LPPLKAESYI 391
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 268 E--SSPHS-----RKALQVKGSTASKDNIIFSLSKKEEYI 301
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

```

```

RESULT      3
US-09-431-367B-5
; Sequence 5, Application US/09431367B
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: NMI-074CP
; CURRENT APPLICATION NUMBER: US/09/431,367B
; CURRENT FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: 09/259,951
; PRIOR FILING DATE: 1999-03-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0

```

```

; SEQ ID NO 5
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-431-367B-5

```

Query Match	18.5%	Score 387	DB Length 332
Best Local Similarity	35.5%	Pred. No. 2.9e-27	
Matches 88	Conservative 51	Mismatches 9	Indels 14
			Gaps 6

[illegible]

```

US-09-798-584-15
? Sequence 15, Application US/09798584
? GENERAL INFORMATION:
? APPLICANT: Mu, David
? APPLICANT: Powers, Scott
? APPLICANT: Tutarik Inc.
? TITLE OF INVENTION: KCNB: A Novel Potassium Channel Protein
? FILE REFERENCE: 018781-004010US
? CURRENT APPLICATION NUMBER: US/09/798,584
? CURRENT FILING DATE: 2001-03-03
? PRIOR APPLICATION NUMBER: US 60/196,951
? PRIOR FILING DATE: 2000-03-03
? NUMBER OF SEQ ID NOS: 18
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 15
? LENGTH: 394
? TYPE: PRT
? ORGANISM: Homo sapiens
? FEATURE:
? OTHER INFORMATION: human potassium channel KCNK3 (TASK1)
US-09-798-584-15

```

```

Query Match 17.7% Score 370; DB Size Length 354;
Best Local Similarity 28.0%; Pred.No. 1.4e-06;
Matches 109; Conservative 66; Mismatches 157; Indels 88; Gaps 13.

OY 42 MKKRVSTFLV--VLYLIIGAAYFKALEQEOEISOR--YVOKSTFACNACVNS--T 97
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 MKRQNRRTALITCYFTYTLTVGCAAFDPALESEPELIERK--ELRQDELARARINLSOGYE 60

OY 98 ELDELQQTVAALIMGIIPLGNSSNOVSHMDLGSSEFF--VTTTIGFCNISPRTEGKI 157
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 ELERVVLR--KPHKAGV-----QMPRAGSEYFE--TGTITGYGHAPSTDGKGV 108

OY 158 ECLIVALLGIPPLFGPLLAACVGDGLGTF-----GK--KVEDFTKNAVSTQIKIKI 208
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 109 ECFMFAVLLGIPPLTVLFVQSLGERINTLVRYLLHRAKKG--L--SAD-----VSM 156

OY 209 ISTIIFIEGCVLFVALPVIPIFKHIEGMSALDAIFVVTITLTIGEGDVVAGGSD--IEY 266

```



	Query Match	16.89;	Score 350.5;	445	Length 258;
	Best Local Similarity	31.28;	Pred. No. 5e-25;		
	Matches	89;	Conservative	60;	Mismatches 89; Indels 45; Gaps
Oy	42 MKKMTVSTFLV--VYLIIIGAFAFALPEOPESITIV QKOTFIADHCAVNSTEL 99				
	: :   :   :		: : : :   :	: :   :	
Db	1 MKRQNVRLAIIVCTFFYLLGAVFALPESEPMIEGRQLPFOLELRARY---NLSEG 57				
Oy	100 D-ELIQIIVAAI---NAGIIPLGNSNOVSOMHDGSSFEFRV VITTFIGNISPRTEGG 155				
	: : :   :	:	:	: :   :	
Db	58 GYEELERLVATLKPHKAGV-----OMRFAGSFVAVITVTIGGHAPSDTGC 106				
Oy	156 KICIFIYAALGIPLFGELAGVGDPOLGTIGCKIAKVELPIKKNNVSQT-----I 206				
	:     :             :	:	:	:	
Db	107 KVPCMFAYALGLPIPLVMFOSLGRIT-----NIIVRYLLRRARRGJGMRAEY 154				



Db 157 ENMTVGFSCMGTLGCAAAAFSGCEEMSFPHAYVYCOTITLTITGFDYVALPTKGALOK 216

Qy 267 LDYKYVYVWFILVGLAFVAVLNMIGMDLRAVSKTKREE--VGEFRAHAA----EWTAN 320

Db 217 KPLVYAFSFMVILGLTVIGAFMLDV--VLEFELTMNSEDEKRDDEERASLAGNMSVVIH 274

Qy 321 VTAEEKERRLLSVEI-----YDKQRATSVYKRKLSAFLAGNHNDLPCR 366

Db 275 IPEEPRRPRPRYKADVPDLQSGVSCCTCYRSODYGGRSVAQNSFSAKLADHYFHSIS--Y 332

Qy 367 RLLSVNHLTSEREVLPLPLKAESIYYLNGLTPH 398

Db 333 KIEELISPTLKNSLFPRSPISISIGLSFIDH 364

```

: RESULT 11
: US-09-431-367b-8
: Sequence 8, Application US/09431367B
: GENERAL INFORMATION:
: APPLICANT: Curtis, Rory A.J
: TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
: FILE REFERENCE: NMI-074CP
: CURRENT APPLICATION NUMBER: US/09/431.367B
: PRIOR FILING DATE: 1999-11-01
: PRIOR APPLICATION NUMBER: 09/259,951
: PRIOR FILING DATE: 1999-03-01
: NUMBER OF SEQ ID NOS: 12
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 8
: LENGTH: 313
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-431-367b-8

```

Query Match	16.4%	Score 342;	DB 5;	Length 313;
Best Local Similarity	34.4%	Pred. No. 4e-24;		
Matches 83;	Conservative 42;	Mismatches 104;	Indels 12;	Gaps 5

```

0Y 117 LGNSNQVS----HMDGSSFEFGATYTTTIGFENISPREGGKIFCIITVALGILPFG 172
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 77 LANASGSANASDPAMDRA$ALFEF$ASTLITTYGYGTYPTLTDAGAF$IAFAL$GVPTML 136
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
0Y 173 LLAGVGDDLTGIFGKGIAKVEDPFIKNNVSQTKIRIISTITFIILFGCVL$VA--LPAVIF 230
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 137 LLT$ASAO$LSL$----LTHVPL$ML$MRGMDPPRAACMHLVALLGVAVVY$C$ELVPAVIF 192
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      231 KHI-EGM$ALDAI$FVVVTTTITIGFQYVAGGSDIE-YLDPKPKVVMFWITL$GL$PAAV 288
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 193 AHLEBAM$F$LD$AF$FC$F$IST$IL$GDVY$PE$AD$G$P$R$AL$Y$K$V$LY$VY$F$LG$IV$AM$V$ 252

```

Qy	289	L	289
		I	
Db	253	L	253

RESULT 12  
US-09-336-643-81  
Sequence 81, Application US/09336643  
GENERAL INFORMATION:  
APPLICANT: Miller, Andrew P.  
APPLICANT: Curran, Mark Edward  
APPLICANT: Hu, Ping  
APPLICANT: Rutter, Marc  
APPLICANT: Wang, Jian-Wang  
TITLE OF INVENTION: Novel Human Potassium Channels  
FILE REFERENCE: SEO-15P  
CURRENT APPLICATION NUMBER: US/09/336,643  
CURRENT FILING DATE: 1999-06-18

```

: PRIOR APPLICATION NUMBER: 60/076,687
: PRIOR FILING DATE: 1998-08-07
: PRIOR APPLICATION NUMBER: 60/116,448
: PRIOR FILING DATE: 1999-01-19
: PRIOR APPLICATION NUMBER: PCT/US99/03826
: PRIOR FILING DATE: 1999-02-22
: NUMBER OF SEQ ID NOS: 87
: SOFTWARE: fastSeq for Windows Version 4.0
: SEQ ID NO 81
: LENGTH: 313
: TYPE: prt
: ORGANISM: H. sapiens
US-09-336-643-81

```

Query Match	16.48	Score	342	DB	1	Length	313
Best Local Similarity	34.48	Pred	No. 4e-2				
Matches	83	Conservative	42	Mismatches	41	Indels	12
						Gaps	5

OY	117	LGNSSNQVS----	HMDLGSFFFGVATYITGFCNINSPH <sup>+</sup>	XIKYIFALLGIPLFGE	1722
		:	:		
Db	77	LANNSSANASDPAMDPA	SALAFESTLITTVGYCTPPLII <sup>+</sup>	3KAF5IAEFLALGVPTTML	1368
OY	173	LLAGVDGLGTIFEGKI	AKAVDEFIKMNVSQTIRIIS <sup>+</sup>	LFGCVLEVA--LPAPIF	230
		:   :	:   :   :	:   :	
Db	137	LITSAQSLSL---	LTHVPLSMLSMRGMDDPRRAICL <sup>+</sup>	LALGVAVTYCETLAPVIF	1922
OY	231	KHI-EGMSALDAIPEVV	TITITIEGFQDVAGSGDIE-YII <sup>+</sup>	KVVVMFIIVGLTAPAAV	2888
		:			
Db	193	AHLBANSFLDAEFCE	TISTLTIGADTVPEAGQPYR <sup>+</sup>	VLYVTIYLFELGVAMVLV	2533

Qy	289 L	289
Db	253 L	253

```

RESULT 13
US-09-431-367B-11
Sequence 11 Application US/09431367B
GENERAL INFORMATION
APPLICANT: CURTIS, RORY A.J
TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL M
FILE REFERENCE: MNI-074CP
CURRENT APPLICATION NUMBER: US/09/431,367B
CURRENT FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: 09/259,951
PRIOR FILING DATE: 1999-03-01
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 401
TYPE: PRT
ORGANISM: Homo sapiens
US-09-431-367B-11

```

Query Match	10.1%	Score 212	DB	Length 401
Best Local Similarity	20.8%	Pred. No. 6.7e-1		
Matches 77; Conservative	37;	Mismatches	172;	Gaps 11

[illegible]

```

Db 150 CMLYALFGLPMLFVLTGDIATLSTSYNPKRPFPTRLSLKWPCKSLFKKKPDP 209
QY 200 ----- 199
Db 210 KPADEAVPQIIISAEELPGKLGCTCPSRSCSMELFERSHAKONTLQLPQAMERSNS 269
QY 200 -----NVSQT-----KIRIISTIIIFGCVLFVALPAVIFKHIEG 235
Db 270 CPELVGLRLSYISINLDEVGQOVERLDIPLPIIALIVFAVISCANAAL-LPF----- 320
QY 236 W-SALD---AIVFVITLTITIGRD-----YVAGSDLEY-----L 267
Db 321 WETQDPENAFYCFVLTITIGFDVLEHPNPFLEFSIYIIVGMETVFAELVONRLI 380
QY 268 DFYKPVVWF 277
Db 381 DIKNWMLPF 390

```

```

RESULT 14
US-09-336-643-16
; Sequence 16, Application US/09336643
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rutler, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: Novel Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/09/336,643
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 197
; TYPE: PRT
; ORGANISM: H. sapiens
US-09-336-643-16

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```

Query Match 7.3%; Score 152.5; DB 5; Length 197;
Best Local Similarity 27.5%; Pred. No. 8.1e-07;
Matches 52; Conservative 39; Mismatches 65; Indels 33; Gaps 8;

```

```

QY 148 ISPRTEGKIFCTIVALLGIFLPGVLDGDLGTFIIFGKIAKVEDTFIKWVSQTKR 207
Db 1 MAPLSPGGAFCFVYALGIPASLALVATLRHCLLPVLSRPRAWVA---VHWQLSPARAA 57
QY 208 IISTIIIFGCVLFVALPAVIFKHIEG-WSALDAIVFVITLTITIGFDYVAG-GSDIE 265
Db 58 LQDAVALGLLVASFVLLPALVLMGLGDCSILGAVYFCSSLSITGLIEDLPLGRGRSLH 117
QY 266 YLDFYRPVWF-----WILGLAYFAVLSMIGDMLRVISKTKREYGEFFRAHAAEW 317
Db 118 -----PVIYHGLQALLGLVLLGL-----LAML-----LAVETFSELPQVRAMGKFF 159
QY 318 --TANYTAE 324
Db 160 RPSGPVTAE 168

```

```

RESULT 15
US-09-760-469-1386
; Sequence 1386, Application US/09760469
; GENERAL INFORMATION:

```

```

; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT254
; CURRENT APPLICATION NUMBER: US/09/760,469
; PRIOR APPLICATION DATA REMOVED - consult PALM file wrapper
; NUMBER OF SEQ ID NOS: 1983
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1386
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-760-469-1386

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Query Match 7.2%; Score 151; DB 5; Length 205;
Best Local Similarity 30.2%; Pred. No. 1.2e-05;
Matches 39; Conservative 28; Mismatches 64; Indels 12; Gaps 6;

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```

QY 197 IKWWSQTKIRIISTII--FILEGCVLFVALPAVIFKHIEG-WSALDAIVFVITLTITIG 253
Db 39 IRMGFSKQVVAIVHVLGFTVYSCFFI--PAVRSVL DDMNPLESFFFCISLSTIG 96
QY 254 FGDYVAG-GSDIEYLDYKPVVWFILVGLAYFAVLSKIGMLRVISK-----KTKREV 307
Db 97 LGDYVPEGEGYNOKFRELYKIGITCYLLGLIAMLVLET CE-LHELKKFRKMFYVKKDK 155
QY 308 GEFRAHAAE 316
Db 156 DEDQVHIIE 164

```

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Search completed: August 28, 2001, 17:11:45
Job time: 389 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 28, 2001, 17:01:11 ; Search time 242.67 Seconds  
(without alignments)  
375.734 Million/cell updates/sec

Title: US-09-503-089A-2

Perfect score: 2100  
Sequence: 1 MAAPDLDPKSAQNSKPRLL.....LNGLPHCAGEEIAVENIK 411

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2803329 segs, 221847457 residues

Total number of hits satisfying chosen parameters: 2803329

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Pending\_Patents\_AA\_Main:\*

1: /cgn2\_6/ptodata/2/paa/PCTUS.COMB.pep:\*  
2: /cgn2\_6/ptodata/2/paa/US06.COMB.pep:\*  
3: /cgn2\_6/ptodata/2/paa/US07.COMB.pep:\*  
4: /cgn2\_6/ptodata/2/paa/US08.COMB.pep:\*  
5: /cgn2\_6/ptodata/2/paa/US081.COMB.pep:\*  
6: /cgn2\_6/ptodata/2/paa/US082.COMB.pep:\*  
7: /cgn2\_6/ptodata/2/paa/US083.COMB.pep:\*  
8: /cgn2\_6/ptodata/2/paa/US084.COMB.pep:\*  
9: /cgn2\_6/ptodata/2/paa/US085.COMB.pep:\*  
10: /cgn2\_6/ptodata/2/paa/US086.COMB.pep:\*  
11: /cgn2\_6/ptodata/2/paa/US087.COMB.pep:\*  
12: /cgn2\_6/ptodata/2/paa/US088.COMB.pep:\*  
13: /cgn2\_6/ptodata/2/paa/US089.COMB.pep:\*  
14: /cgn2\_6/ptodata/2/paa/US090.COMB.pep:\*  
15: /cgn2\_6/ptodata/2/paa/US091.COMB.pep:\*  
16: /cgn2\_6/ptodata/2/paa/US092.COMB.pep:\*  
17: /cgn2\_6/ptodata/2/paa/US093.COMB.pep:\*  
18: /cgn2\_6/ptodata/2/paa/US094.COMB.pep:\*  
19: /cgn2\_6/ptodata/2/paa/US095.COMB.pep:\*  
20: /cgn2\_6/ptodata/2/paa/US096.COMB.pep:\*  
21: /cgn2\_6/ptodata/2/paa/US097.COMB.pep:\*  
22: /cgn2\_6/ptodata/2/paa/US098.COMB.pep:\*  
23: /cgn2\_6/ptodata/2/paa/US099.COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2100	100.0	411	19 US-09-503-089A-2	Sequence 2, Appl
2	2095	99.8	411	1 PCT-US99-03826-83	Sequence 83, Appl
3	2095	99.8	411	17 US-09-336-643-83	Sequence 83, Appl
4	2095	99.8	411	17 US-09-336-643-83	Sequence 83, Appl
5	2095	99.8	411	22 US-09-828-746-2	Sequence 2, Appl
6	2062	98.2	426	12 US-08-816-011-45	Sequence 45, Appl
7	2062	98.2	426	12 US-08-816-011A-45	Sequence 45, Appl
8	2062	98.2	426	12 US-08-816-011C-45	Sequence 45, Appl
9	2041	97.2	411	19 US-09-503-089A-4	Sequence 4, Appl
10	2035	96.9	411	22 US-09-828-746-6	Sequence 6, Appl

11	1833	87.3	370	20 US-09-655-272-4	Sequence 4, Appl
12	1824	86.9	370	15 US-09-144-914-8	Sequence 8, Appl
13	1824	86.9	370	18 US-09-436-265-8	Sequence 8, Appl
14	1243	59.2	543	1 PCT-US01-14965-73	Sequence 73, Appl
15	1243	59.2	543	22 US-09-852-386-73	Sequence 73, Appl
16	1241.5	59.1	657	23 US-60-207-583-37	Sequence 376, Appl
17	1215.5	57.9	724	23 US-60-216-547-10	Sequence 10, Appl
18	1205	57.4	484	23 US-60-230-445-17	Sequence 1632, Ap
19	803	38.2	392	1 PCT-US00-34983-	Sequence 55, Appl
20	803	38.2	392	21 US-09-729-739-	Sequence 55, Appl
21	803	38.2	392	18 US-09-432-470-	Sequence 2, Appl
22	803	38.2	393	18 US-09-432-470-6	Sequence 2, Appl
23	803	38.2	419	22 US-09-828-035-	Sequence 4, Appl
24	803	38.2	440	23 US-60-258-275-5	Sequence 424, App
25	803	38.2	1314	1 PCT-US00-34983-	Sequence 29, Appl
26	803	38.2	1314	21 US-09-729-739-	Sequence 29, Appl
27	776.5	37.0	398	20 US-09-655-272-	Sequence 2, Appl
28	759.5	36.2	1779	23 US-60-212-358-1	Sequence 133, App
29	759.5	36.2	1785	23 US-60-207-416-9	Sequence 91, Appl
30	758	36.1	1616	23 US-60-229-525-3-1	Sequence 331, App
31	638.5	30.4	1068	23 US-60-212-358-1-5	Sequence 195, Appl
32	547	26.0	107	22 US-09-828-746-6	Sequence 4, Appl
33	519	24.7	110	23 US-60-171-487-5	Sequence 594, App
34	513	24.4	295	23 US-60-223-269-8	Sequence 8, Appl
35	427	20.3	499	16 US-09-259-951-2	Sequence 2, Appl
36	427	20.3	499	16 US-09-259-951-4	Sequence 4, Appl
37	427	20.3	499	17 US-09-357-425-6	Sequence 6, Appl
38	427	20.3	499	18 US-09-436-265-7	Sequence 28, Appl
39	427	20.3	499	19 US-09-561-763-	Sequence 2, Appl
40	427	20.3	499	21 US-09-735-169-4	Sequence 2, Appl
41	427	20.3	499	21 US-09-735-169-4	Sequence 4, Appl
42	427	20.3	499	21 US-09-735-169A-	Sequence 2, Appl
43	427	20.3	499	21 US-09-735-171-2	Sequence 2, Appl
44	427	20.3	499	21 US-09-735-171-4	Sequence 4, Appl
45	427	20.3	499	21 US-09-735-171A-2	Sequence 2, Appl

#### ALIGNMENTS

RESULT 1  
US-09-503-089A-2  
; Sequence 2, Application US/09503089A  
; GENERAL INFORMATION:  
; APPLICANT: PATEL, AMANDA J.  
; APPLICANT: HONORE, ERIC  
; APPLICANT: LESAGE, FLORIAN  
; APPLICANT: ROMER, GEORGES  
; APPLICANT: LAZDOSKI, MICHEL  
; TITLE OF INVENTION: A method for the identification of anesthetics  
; FILE REFERENCE: f1b12prov3-humanantrex  
; CURRENT APPLICATION NUMBER: US/09/503,089A  
; CURRENT FILING DATE: 2000-02-11  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: Microsoft Word 2000  
; SEQ ID NO 2  
; LENGTH: 411  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-503-089A-2

Query Match	100.0%	Score 2100;	E 19;	Length 411;
Best Local Similarity	100.0%	Pred. No. 1.6;	03;	Indels 0;
Matches 411;	Conservative 0;	Mismatches 0;	Gaps 0;	
QY	1	MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESDTT1	MAKTIVSTFTLVVLYLII 60	
DB	1	MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESDTT1	MAKTIVSTFTLVVLYLII 60	
QY	61	GATVFALEQPHISORTTIVIOKOTFISGHCVNSTEL	LLIOQIVAAINAGIIPLGNT 120	
DB	61	GATVFALEQPHISORTTIVIOKOTFISGHCVNSTEL	LLIOQIVAAINAGIIPLGNT 120	

```

OY 121 SNOISHMDLSSFFAGTIVTTIGFNGISPRTEGKIFCIYALLGIPLEFGLAGVGO 180
DB 121 SNOISHMDLSSFFAGTIVTTIGFNGISPRTEGKIFCIYALLGIPLEFGLAGVGO 180
OY 181 LGTIFGKGIKAKVEDPFIKNNVSQTKIRIISTIIIFILFGCVLPAALPIFKHIEGMSALD 240
DB 181 LGTIFGKGIKAKVEDPFIKNNVSQTKIRIISTIIIFILFGCVLPAALPIFKHIEGMSALD 240
OY 241 AIYFVYITLTITGFGDYVAGSDIEYLDYFKPVWFMWILVGLAFYFAAVLSMIGDMLRVIS 300
DB 241 AIYFVYITLTITGFGDYVAGSDIEYLDYFKPVWFMWILVGLAFYFAAVLSMIGDMLRVIS 300
OY 301 KKTKEEYGEFRAHAEMTANVTAEFKETRRLSVEIYDKFORATSIKRLSALAGNHNQ 360
DB 301 KKTKEEYGEFRAHAEMTANVTAEFKETRRLSVEIYDKFORATSIKRLSALAGNHNQ 360
OY 361 ELTPCRRITLSVNHILTNERDVLPLPLKTESIYLANGLTPHCAGEIYAVIENIK 411
DB 361 ELTPCRRITLSVNHILTNERDVLPLPLKTESIYLANGLTPHCAGEIYAVIENIK 411

```

## RESULT 2

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PCT-US99-03826-83
; Sequence 83, Application PC/TUS9903826A
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew
; APPLICANT: Curran, Mark
; TITLE OF INVENTION: Novel Human Potassium Channels
; FILE REFERENCE: SEQ-15PCT
; CURRENT APPLICATION NUMBER: PCT/US99/03826A
; EARLIER FILING DATE: 1999-02-22
; EARLIER APPLICATION NUMBER: 60/076,687
; EARLIER FILING DATE: 1998-02-25
; EARLIER APPLICATION NUMBER: 60/095,836
; EARLIER FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: 60/116,448
; EARLIER FILING DATE: 1999-01-19
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 83
; LENGTH: 411
; TYPE: PRT
; ORGANISM: H. sapiens
PCT-US99-03826-83

```

Query Match 99.8%; Score 2095; DB 1; Length 411;

Best Local Similarity 99.8%; Pred. No. 5.2e-203;

Matches 410; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 MAAPDLDPKSAONSKPRLSFTKPTVLASRVESDTITVMAKTVSTIFLVVLYLIT 60
DB 1 MAAPDLDPKSAONSKPRLSFTKPTVLASRVESDTITVMAKTVSTIFLVVLYLIT 60
OY 61 GATVFALKEPHEISORTIVIVOKOTFISQHSVCNSTEDELIOQIYAAINAGIIPLGNT 120
DB 61 GATVFALKEPHEISORTIVIVOKOTFISQHSVCNSTEDELIOQIYAAINAGIIPLGNT 120
OY 121 SNOISHMDLSSFFAGTIVTTIGFNGISPRTEGKIFCIYALLGIPLEFGLAGVGO 180
DB 121 SNOISHMDLSSFFAGTIVTTIGFNGISPRTEGKIFCIYALLGIPLEFGLAGVGO 180
OY 181 LGTIFGKGIKAKVEDPFIKNNVSQTKIRIISTIIIFILFGCVLPAALPIFKHIEGMSALD 240
DB 181 LGTIFGKGIKAKVEDPFIKNNVSQTKIRIISTIIIFILFGCVLPAALPIFKHIEGMSALD 240
OY 241 AIYFVYITLTITGFGDYVAGSDIEYLDYFKPVWFMWILVGLAFYFAAVLSMIGDMLRVIS 300
DB 241 AIYFVYITLTITGFGDYVAGSDIEYLDYFKPVWFMWILVGLAFYFAAVLSMIGDMLRVIS 300
OY 301 KKTKEEYGEFRAHAEMTANVTAEFKETRRLSVEIYDKFORATSIKRLSALAGNHNQ 360
DB 301 KKTKEEYGEFRAHAEMTANVTAEFKETRRLSVEIYDKFORATSIKRLSALAGNHNQ 360

```

```

DB 301 KKTKEEYGEFRAHAEMTANVTAEFKETRRLSVEIYDKFORATSIKRLSALAGNHNQ 360
OY 361 ELTPCRRITLSVNHILTNERDVLPLPLKTESIYLANGLTPHCAGEIYAVIENIK 411
DB 361 ELTPCRRITLSVNHILTNERDVLPLPLKTESIYLANGLTPHCAGEIYAVIENIK 411

```

## RESULT 3

```

US-09-336-643-83
; Sequence 83, Application US/09336643
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew
; APPLICANT: Curran, Mark
; APPLICANT: Ping Hu
; APPLICANT: Marc Rutter
; APPLICANT: Jian-Ying Wang
; TITLE OF INVENTION: Novel Human Potassium Cha
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/09/336,643
; EARLIER FILING DATE: 1999-06-18
; EARLIER APPLICATION NUMBER: 60/095,836
; EARLIER FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: 60/116,448
; EARLIER FILING DATE: 1999-01-19
; EARLIER APPLICATION NUMBER: PCT/US99/03826
; EARLIER FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 83
; LENGTH: 411
; TYPE: PRT
; ORGANISM: H. sapiens
US-09-336-643-83

```

Query Match 99.8%; Score 2095; DB 1; Length 411;

Best Local Similarity 99.8%; Pred. No. 5.2e-203;

Matches 410; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 MAAPDLDPKSAONSKPRLSFTKPTVLASRVESDTITVMAKTVSTIFLVVLYLIT 60
DB 1 MAAPDLDPKSAONSKPRLSFTKPTVLASRVESDTITVMAKTVSTIFLVVLYLIT 60
OY 61 GATVFALKEPHEISORTIVIVOKOTFISQHSVCNSTEDELIOQIYAAINAGIIPLGNT 120
DB 61 GATVFALKEPHEISORTIVIVOKOTFISQHSVCNSTEDELIOQIYAAINAGIIPLGNT 120
OY 121 SNOISHMDLSSFFAGTIVTTIGFNGISPRTEGKIFCIYALLGIPLEFGLAGVGO 180
DB 121 SNOISHMDLSSFFAGTIVTTIGFNGISPRTEGKIFCIYALLGIPLEFGLAGVGO 180
OY 181 LGTIFGKGIKAKVEDPFIKNNVSQTKIRIISTIIIFILFGCVLPAALPIFKHIEGMSALD 240
DB 181 LGTIFGKGIKAKVEDPFIKNNVSQTKIRIISTIIIFILFGCVLPAALPIFKHIEGMSALD 240
OY 241 AIYFVYITLTITGFGDYVAGSDIEYLDYFKPVWFMWILVGLAFYFAAVLSMIGDMLRVIS 300
DB 241 AIYFVYITLTITGFGDYVAGSDIEYLDYFKPVWFMWILVGLAFYFAAVLSMIGDMLRVIS 300
OY 301 KKTKEEYGEFRAHAEMTANVTAEFKETRRLSVEIYDKFORATSIKRLSALAGNHNQ 360
DB 301 KKTKEEYGEFRAHAEMTANVTAEFKETRRLSVEIYDKFORATSIKRLSALAGNHNQ 360
OY 361 ELTPCRRITLSVNHILTNERDVLPLPLKTESIYLANGLTPHCAGEIYAVIENIK 411
DB 361 ELTPCRRITLSVNHILTNERDVLPLPLKTESIYLANGLTPHCAGEIYAVIENIK 411

```

## RESULT 4

```

US-09-336-643-83
; Sequence 83, Application US/09336643A
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.

```



```

; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rutter, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: Novel Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/09/336,643A
; CURRENT FILING DATE: 1999-06-18
; EARLIER APPLICATION NUMBER: 60/076,687
; EARLIER FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: 60/116,448
; EARLIER FILING DATE: 1999-01-19
; EARLIER APPLICATION NUMBER: PCT/US99/03826
; EARLIER FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 411
; TYPE: PRT
; ORGANISM: H. sapiens
US-09-336-643-83

```

```

Query Match          99.8%; Score 2095; DB 17; Length 411;
Best Local Similarity 99.8%; Pred. No. 5.2e-203;
Matches 410; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MAADLLDPKSAONSKRPLSFSTRKPTVLASRVESDPTINVMKKKTVSTIFLVVLYLI 60
DB 1 MAADLLDPKSAONSKRPLSFSTRKPTVLASRVESDPTINVMKKKTVSTIFLVVLYLI 60
QY 61 GATVFKALEOPHEISORTTIVIOKOTFISQHCYNSTELDELIOOYVAIINAGIIPLGNT 120
DB 61 GATVFKALEOPHEISORTTIVIOKOTFISQHCYNSTELDELIOOYVAIINAGIIPLGNT 120
QY 121 SNOISHMDLGSSFFAGTIVITIGFGNISPRTBEGKIFCIITIALGIPFGLAGVDQ 180
DB 121 SNOISHMDLGSSFFAGTIVITIGFGNISPRTBEGKIFCIITIALGIPFGLAGVDQ 180
QY 121 SNOISHMDLGSSFFAGTIVITIGFGNISPRTBEGKIFCIITIALGIPFGLAGVDQ 180
DB 121 SNOISHMDLGSSFFAGTIVITIGFGNISPRTBEGKIFCIITIALGIPFGLAGVDQ 180
QY 181 LGTIFGKIAKVEDPTFKMNSQTKIRIISTIFILFCGVFVALPAIIFKHIGWSALD 240
DB 181 LGTIFGKIAKVEDPTFKMNSQTKIRIISTIFILFCGVFVALPAIIFKHIGWSALD 240
QY 241 AIYFVITLTITIGFDYVAGSDIEYLDYKPYVMFWLVLGAYFAVLSMIGMLRVIS 300
DB 241 AIYFVITLTITIGFDYVAGSDIEYLDYKPYVMFWLVLGAYFAVLSMIGMLRVIS 300
QY 301 KKTKEEVEGFRAHAEMTANTATAEKTRRLSVEIYDKQIRATSIKRLSAELAGNHQ 360
DB 301 KKTKEEVEGFRAHAEMTANTATAEKTRRLSVEIYDKQIRATSIKRLSAELAGNHQ 360
QY 361 ELTPCRRTLSVNHLTNERDVLPLPKTESIYLNGLTPHCAGEETAVIENIK 411
DB 361 ELTPCRRTLSVNHLTNERDVLPLPKTESIYLNGLTPHCAGEETAVIENIK 411

```

```

RESULT 5
US-09-828-746-2
; Sequence 2, Application US/09828746
; GENERAL INFORMATION:
; APPLICANT: Helen Jane Meadows
; APPLICANT: Conrad Gerald Chapman
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30031-D1
; CURRENT APPLICATION NUMBER: US/09/828,746
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: US 09/236,080
; PRIOR FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: EP 98300570.3
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: UK 9822135.1
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 6

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26020625485

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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 411
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-828-746-2

```

```

Query Match          99.8%; Score 2095; DB 42; Length 411;
Best Local Similarity 99.8%; Pred. No. 5.2e-43;
Matches 410; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MAADLLDPKSAONSKRPLSFSTRKPTVLASRVESDPTINVMKKKTVSTIFLVVLYLI 60
DB 1 MAADLLDPKSAONSKRPLSFSTRKPTVLASRVESDPTINVMKKKTVSTIFLVVLYLI 60
QY 61 GATVFKALEOPHEISORTTIVIOKOTFISQHCYNSTELDELIOOYVAIINAGIIPLGNT 120
DB 61 GATVFKALEOPHEISORTTIVIOKOTFISQHCYNSTELDELIOOYVAIINAGIIPLGNT 120
QY 121 SNOISHMDLGSSFFAGTIVITIGFGNISPRTBEGKIFCIITIALGIPFGLAGVDQ 180
DB 121 SNOISHMDLGSSFFAGTIVITIGFGNISPRTBEGKIFCIITIALGIPFGLAGVDQ 180
QY 181 LGTIFGKIAKVEDPTFKMNSQTKIRIISTIFILFCGVFVALPAIIFKHIGWSALD 240
DB 181 LGTIFGKIAKVEDPTFKMNSQTKIRIISTIFILFCGVFVALPAIIFKHIGWSALD 240
QY 241 AIYFVITLTITIGFDYVAGSDIEYLDYKPYVMFWLVLGAYFAVLSMIGMLRVIS 300
DB 241 AIYFVITLTITIGFDYVAGSDIEYLDYKPYVMFWLVLGAYFAVLSMIGMLRVIS 300
QY 301 KKTKEEVEGFRAHAEMTANTATAEKTRRLSVEIYDKQIRATSIKRLSAELAGNHQ 360
DB 301 KKTKEEVEGFRAHAEMTANTATAEKTRRLSVEIYDKQIRATSIKRLSAELAGNHQ 360
QY 361 ELTPCRRTLSVNHLTNERDVLPLPKTESIYLNGLTPHCAGEETAVIENIK 411
DB 361 ELTPCRRTLSVNHLTNERDVLPLPKTESIYLNGLTPHCAGEETAVIENIK 411

```

```

RESULT 6
US-08-816-011-45
; Sequence 45, Application US/08816011
; GENERAL INFORMATION:
; APPLICANT: Price, Laura A.
; APPLICANT: Pausch, Mark H.
; TITLE OF INVENTION: Potassium Channels, Nucleotide Sequences
; TITLE OF INVENTION: Encoding Them, and Methods of Using Same
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Home Products Corporation
; STREET: One Campus Drive
; CITY: Parsippany
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version 1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/816,011
; FILING DATE: 11-MAR-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Matthews, Gale F.
; REGISTRATION NUMBER: 32,269
; REFERENCE/DOCKET NUMBER: 32,421-C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-683-2134
; TELEFAX: 201-683-4117

```

20030165806

```

; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 426 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-816-011-45

```

```

Query Match      98.2%; Score 2062; DB 12; Length 426;
Best Local Similarity 98.5%; Pred. No. 1.2e-199;
Matches 405; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 1 MAAPDLDPKSAQNSKPRLSSTKPTVLASRVESDTTINVMKKTIVSTFLVVLXLI 60
; :|||||
DB 16 VAAPDLDPKSAQNSKPRLSSTKPTVLASRVESDTTINVMKKTIVSTFLVVLXLI 75
QY 61 GATVFKALEQPHIEISORTTIVIOKQTFISQHSQVNSTELDELIOQIVAAINAGIIPLGNT 120
; :|||||
DB 76 GATVFKALEQPHIEISORTTIVIOKQTFISQHSQVNSTELDELIOQIVAAINAGIIPLGNT 135
QY 121 SNOISHMDLGSFFPAGTIVTTIGFQNISPRTEGKIFCIIYALGLPLFGFLLAGVDQ 180
; :|||||
DB 136 SNOISHMDLGSFFPAGTIVTTIGFQNISPRTEGKIFCIIYALGLPLFGFLLAGVDQ 195
QY 181 LGTIFGKIAKVEDTIFKMNVSOTKIRIISTIFILFGCVLFPALPAIFKHIEGMSALD 240
; :|||||
DB 196 LGTIFGKIAKVEDTIFKMNVSOTKIRIISTIFILFGCVLFPALPAIFKHIEGMSALD 255
QY 241 AIFVAVITLTTFGFDYVAGSDIEYLDYKPYVMFWILVGLAFPAVLSMIGRLVVIS 300
; :|||||
DB 256 AIFVAVITLTTFGFDYVAGSDIEYLDYKPYVMFWILVGLAFPAVLSMIGRLVVIS 315
QY 301 KTKKEVGEFRHAAEMTANVTAEFKETRRRLSVEIYDKFORATSIKRLSAELAGNHQ 360
; :|||||
DB 316 KTKKEVGEFRHAAEMTANVTAEFKETRRRLSVEIYDKFORATSIKRLSAELAGNHQ 375
QY 361 ELTPCRRTLSVNHLTNERDVLPLPLKTESIYNGLTPHCGEEIAVENIK 411
; :|||||
DB 376 ELTPCRRTLSVNHLTNERDVLPLPLKTESIYNGLTPHCGEEIAVENIK 426

```

```

RESULT 7
US-08-816-011A-45
; Sequence 45, Application US/08816011A
; GENERAL INFORMATION:
; APPLICANT: Price, Laura A.
; APPLICANT: Pausch, Mark H.
; TITLE OF INVENTION: Potassium Channels, Nucleotide Sequences
; TITLE OF INVENTION: Encoding Them, and Methods of Using Same
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Home Products Corporation
; STREET: One Campus Drive
; CITY: Parsippany
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/816,011A
; FILING DATE: 11-MAR-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Matthews, Gale F.
; REGISTRATION NUMBER: 32,269
; REFERENCE/DOCKET NUMBER: 32,421-C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-683-2134

```

```

; TELEFAX: 201-683-4117
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 426 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-816-011A-45

```

```

Query Match      98.2%; Score 2062; DB 12; Length 426;
Best Local Similarity 98.5%; Pred. No. 1.2e-199;
Matches 405; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 1 MAAPDLDPKSAQNSKPRLSSTKPTVLASRVESDTTINVMKKTIVSTFLVVLXLI 60
; :|||||
DB 16 VAAPDLDPKSAQNSKPRLSSTKPTVLASRVESDTTINVMKKTIVSTFLVVLXLI 75
QY 61 GATVFKALEQPHIEISORTTIVIOKQTFISQHSQVNSTELDELIOQIVAAINAGIIPLGNT 120
; :|||||
DB 76 GATVFKALEQPHIEISORTTIVIOKQTFISQHSQVNSTELDELIOQIVAAINAGIIPLGNT 135
QY 121 SNOISHMDLGSFFPAGTIVTTIGFQNISPRTEGKIFCIIYALGLPLFGFLLAGVDQ 180
; :|||||
DB 136 SNOISHMDLGSFFPAGTIVTTIGFQNISPRTEGKIFCIIYALGLPLFGFLLAGVDQ 195
QY 181 LGTIFGKIAKVEDTIFKMNVSOTKIRIISTIFILFGCVLFPALPAIFKHIEGMSALD 240
; :|||||
DB 196 LGTIFGKIAKVEDTIFKMNVSOTKIRIISTIFILFGCVLFPALPAIFKHIEGMSALD 255
QY 241 AIFVAVITLTTFGFDYVAGSDIEYLDYKPYVMFWILVGLAFPAVLSMIGRLVVIS 300
; :|||||
DB 256 AIFVAVITLTTFGFDYVAGSDIEYLDYKPYVMFWILVGLAFPAVLSMIGRLVVIS 315
QY 301 KTKKEVGEFRHAAEMTANVTAEFKETRRRLSVEIYDKFORATSIKRLSAELAGNHQ 360
; :|||||
DB 316 KTKKEVGEFRHAAEMTANVTAEFKETRRRLSVEIYDKFORATSIKRLSAELAGNHQ 375
QY 361 ELTPCRRTLSVNHLTNERDVLPLPLKTESIYNGLTPHCGEEIAVENIK 411
; :|||||
DB 376 ELTPCRRTLSVNHLTNERDVLPLPLKTESIYNGLTPHCGEEIAVENIK 426

```

```

RESULT 8
US-08-816-011C-45
; Sequence 45, Application US/08816011C
; GENERAL INFORMATION:
; APPLICANT: Price, Laura A.
; APPLICANT: Pausch, Mark H.
; TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,
; TITLE OF INVENTION: AND METHODS OF USING SAME
; FILE REFERENCE: 01142, 0122 SEQUENCE LISTING
; CURRENT APPLICATION NUMBER: US/08/816,011C
; CURRENT FILING DATE: 1997-03-11
; PRIOR APPLICATION NUMBER: 08/332,312
; PRIOR FILING DATE: 1994-10-31
; PRIOR APPLICATION NUMBER: PCF/US95/14364
; PRIOR FILING DATE: 1995-10-25
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 45
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-816-011C-45

```

```

Query Match      98.2%; Score 2062; DB 12; Length 426;
Best Local Similarity 98.5%; Pred. No. 1.2e-199;
Matches 405; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 MAAPDLDPKSAQNSKPRLSSTKPTVLASRVESDTTINVMKKTIVSTFLVVLXLI 60
; :|||||

```

```

Db 16 VAAFDLDPKSAONSKRSLFSFTRPVLASRVESDTTINVMKKTSTIFLVVLYLII 75
QY 61 GATVFAKALPOHEISORTTIVIOKOTFISOHSCVNSTELDELIOOVAIINAGIIPLGNT 120
Db 76 GATVFAKALPOHEISORTTIVIOKOTFISOHSCVNSTELDELIOOVAIINAGIIPLGNT 135
QY 121 SNOISHMDLSSFFPAGTIVITTTIGFNGISPRTEGKIFCIIYALLGIPLFGLAGVGDQ 180
Db 136 SNOISHMDLSSFFPAGTIVITTTIGFNGISPRTEGKIFCIIYALLGIPLFGLAGVGDQ 195
QY 181 LGTIFGKIAVEDTFFIKMNSQTKIRIISITIFLFGCVLFVALPAIIFKHIGBSALD 240
Db 196 LGTIFGKIAVEDTFFIKMNSQTKIRIISITIFLFGCVLFVALPAIIFKHIGBSALD 255
QY 241 AIFVVIITLTITIGFDYVAGSDIEYDFKPVVFWMLVGLAFAAVLSMIGMLRVIS 300
Db 256 AIFVVIITLTITIGFDYVAGSDIEYDFKPVVFWMLVGLAFAAVLSMIGMLRVIS 315
QY 301 KKTKEEVEGFRAHAAEMWTANYTAEFKETRRLRSVEIYDKFORATSIKRLSAELAGNHQ 360
Db 316 KKTKEEVEGFRAHAAEMWTANYTAEFKETRRLRSVEIYDKFORATSIKRLSAELAGNHQ 375
QY 361 ELTPCRRLSVNHLTNERDVPPLKTESIYLNGLPHCAEELAVIENIK 411
Db 376 ELTPCRRLSVNHLTNERDVPPLKTESIYLNGLPHCAEELAVIENIK 426

```

## RESULT 9

US-09-503-089a-4

```

: Sequence 4, Application US/09503089a
: GENERAL INFORMATION:
: APPLICANT: PATEL, AMANDA J.
: APPLICANT: HONORE, ERIC
: APPLICANT: LESAGE, FLORIAN
: APPLICANT: ROMERY, GEORGES
: APPLICANT: LAZDUSKI, MICHEL
: TITLE OF INVENTION: A method for the identification of anesthetics
: FILE REFERENCE: F17B12prov3-humanATREK
: CURRENT APPLICATION NUMBER: US/09/503,089a
: CURRENT FILING DATE: 2000-02-11
: NUMBER OF SEQ ID NOS: 5
: SOFTWARE: Microsoft Word 2000
: SEQ ID NO 4
: LENGTH: 411
: TYPE: PRT
: ORGANISM: Mus musculus
US-09-503-089a-4

```

```

Query Match 97.2%; Score 2041; DB 19; Length 411;
Best Local Similarity 96.1%; Pred. No. 1.6e-197;
Matches 395; Conservative 12; Mismatches 4; Indels 0; Gaps 0;

```

```

QY 1 MAAPDLDPKSAONSKRSLFSFTRPVLASRVESDTTINVMKKTSTIFLVVLYLII 60
Db 1 MAAPDLDPKSAONSKRSLFSFTRPVLASRVESDTTINVMKKTSTIFLVVLYLII 60
QY 61 GATVFAKALPOHEISORTTIVIOKOTFISOHSCVNSTELDELIOOVAIINAGIIPLGNT 120
Db 61 GATVFAKALPOHEISORTTIVIOKOTFISOHSCVNSTELDELIOOVAIINAGIIPLGNT 120
QY 121 SNOISHMDLSSFFPAGTIVITTTIGFNGISPRTEGKIFCIIYALLGIPLFGLAGVGDQ 180
Db 121 SNOISHMDLSSFFPAGTIVITTTIGFNGISPRTEGKIFCIIYALLGIPLFGLAGVGDQ 180
QY 181 LGTIFGKIAVEDTFFIKMNSQTKIRIISITIFLFGCVLFVALPAIIFKHIGBSALD 240
Db 181 LGTIFGKIAVEDTFFIKMNSQTKIRIISITIFLFGCVLFVALPAIIFKHIGBSALD 240
QY 241 AIFVVIITLTITIGFDYVAGSDIEYDFKPVVFWMLVGLAFAAVLSMIGMLRVIS 300
Db 241 AIFVVIITLTITIGFDYVAGSDIEYDFKPVVFWMLVGLAFAAVLSMIGMLRVIS 300

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```

QY 301 KKTKEEVEGFRAHAAEMWTANYTAEFKETRRLRSVEIYDK 360
Db 301 KKTKEEVEGFRAHAAEMWTANYTAEFKETRRLRSVEIYDK 360
QY 361 ELTPCRRLSVNHLTNERDVPPLKTESIYLNGLTPHC 411
Db 361 ELTPCRRLSVNHLTNERDVPPLKTESIYLNGLTPHC 411

```

## RESULT 10

US-09-828-746-6

```

: Sequence 6, Application US/09828746
: GENERAL INFORMATION:
: APPLICANT: Helen Jane Meadows
: APPLICANT: Conrad Gerald Chapman
: TITLE OF INVENTION: NOVEL COMPOUNDS
: FILE REFERENCE: GP-30031-D1
: CURRENT APPLICATION NUMBER: US/09/828,746
: PRIOR FILING DATE: 1999-04-09
: PRIOR APPLICATION NUMBER: US 09/236,080
: PRIOR FILING DATE: 1999-01-25
: PRIOR APPLICATION NUMBER: EP 98300570.3
: PRIOR FILING DATE: 1998-01-27
: PRIOR APPLICATION NUMBER: UK 9822135.1
: PRIOR FILING DATE: 1998-10-09
: NUMBER OF SEQ ID NOS: 6
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 6
: LENGTH: 411
: TYPE: PRT
: ORGANISM: HOMO SAPIENS
US-09-828-746-6

```

```

Query Match 96.9%; Score 2035; DB 19; Length 411;
Best Local Similarity 95.9%; Pred. No. 6.3e-197;
Matches 394; Conservative 12; Mismatches 4; Indels 0; Gaps 0;

```

```

QY 1 MAAPDLDPKSAONSKRSLFSFTRPVLASRVESDTTINVMKKTSTIFLVVLYLII 60
Db 1 MAAPDLDPKSAONSKRSLFSFTRPVLASRVESDTTINVMKKTSTIFLVVLYLII 60
QY 61 GATVFAKALPOHEISORTTIVIOKOTFISOHSCVNSTELDELIOOVAIINAGIIPLGNT 120
Db 61 GATVFAKALPOHEISORTTIVIOKOTFISOHSCVNSTELDELIOOVAIINAGIIPLGNT 120
QY 121 SNOISHMDLSSFFPAGTIVITTTIGFNGISPRTEGKIFCIIYALLGIPLFGLAGVGDQ 180
Db 121 SNOISHMDLSSFFPAGTIVITTTIGFNGISPRTEGKIFCIIYALLGIPLFGLAGVGDQ 180
QY 181 LGTIFGKIAVEDTFFIKMNSQTKIRIISITIFLFGCVLFVALPAIIFKHIGBSALD 240
Db 181 LGTIFGKIAVEDTFFIKMNSQTKIRIISITIFLFGCVLFVALPAIIFKHIGBSALD 240
QY 241 AIFVVIITLTITIGFDYVAGSDIEYDFKPVVFWMLVGLAFAAVLSMIGMLRVIS 300
Db 241 AIFVVIITLTITIGFDYVAGSDIEYDFKPVVFWMLVGLAFAAVLSMIGMLRVIS 300
QY 301 KKTKEEVEGFRAHAAEMWTANYTAEFKETRRLRSVEIYDK 360
Db 301 KKTKEEVEGFRAHAAEMWTANYTAEFKETRRLRSVEIYDK 360
QY 361 ELTPCRRLSVNHLTNERDVPPLKTESIYLNGLTPHC 411
Db 361 ELTPCRRLSVNHLTNERDVPPLKTESIYLNGLTPHC 411

```

## RESULT 11

US-09-655-272-4

```

: Sequence 4, Application US/09655272
: GENERAL INFORMATION:
: APPLICANT: HONORE, ERIC
: APPLICANT: FINK, MICHEL

```

0.447

```
APPLICANT: LAZDUNSKI, MICHEL
APPLICANT: LESAGE, FLORIAN
APPLICANT: DUPRAT, FABRICE
TITLE OF INVENTION: MECHANOSENSITIVE MAMMALIAN POTASSIUM CHANNELS
TITLE OF INVENTION: ACTIVATABLE BY POLYUNSATURATED FATTY ACIDS AND THE USE
FILE REFERENCE: 1383-00
CURRENT APPLICATION NUMBER: US/09/655,272
CURRENT FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: PCT/FR99/00404
PRIOR FILING DATE: 1999-02-23
PRIOR APPLICATION NUMBER: FR 98/02725
PRIOR FILING DATE: 1998-03-05
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 370
TYPE: PRT
ORGANISM: Unknown Sequence
FEATURE:
OTHER INFORMATION: Description of Unknown Sequence: TREK
US-09-655-272-4
```

```
Query Match      87.3% Score 1833; DB 20; Length 370;
Best Local Similarity 96.7%; Pred. No. 1.7e-176;
Matches 356; Conservative 8; Mismatches 4; Indels 0; Gaps 0;
```

```
OY 1 MAAPDLDPKSAONSKPRLSFTKPTVLASRVESDPTTNVKKMKTSTFLVVLXLI 60
DB 1 MAAPDLDPKSAONSKPRLSFTKPTVLASRVESDPTTNVKKMKTSTFLVVLXLI 60
OY 61 GAVFKALEQPEISORTTIVIOKOTFISQHCVNSTEDELIOQIVAAINAGIPLGNT 120
DB 61 GAVFKALEQPEISORTTIVIOKOTFISQHCVNSTEDELIOQIVAAINAGIPLGNS 120
OY 121 SNOISHMDLSSFFAGVTITIGFNGISPRTEGKIFCIYALLGIPLEGFLAGVGDO 180
DB 121 SNOISHMDLSSFFAGVTITIGFNGISPRTEGKIFCIYALLGIPLEGFLAGVGDO 180
OY 181 LGTFEKGIAKVEDTPIKNNVSQTKIRIISTIFILFGCVLPAVLFKHIEGMSALD 240
DB 181 LGTFEKGIAKVEDTPIKNNVSQTKIRIISTIFILFGCVLPAVLFKHIEGMSALD 240
OY 241 AIYFVYITLTITIGFDYVAGSDIEYLDYKPYVWFMIILGLAYFAVLSMIGDMLRVIS 300
DB 241 AIYFVYITLTITIGFDYVAGSDIEYLDYKPYVWFMIILGLAYFAVLSMIGDMLRVIS 300
OY 301 KTKKEVGEFRAHAAMTANVTAEFKETRRRLSVEIYDKFORATSIKRLSALAGNHNQ 360
DB 301 KTKKEVGEFRAHAAMTANVTAEFKETRRRLSVEIYDKFORATSIKRLSALAGNHNQ 360
OY 361 ELTPCART 368
DB 361 ELTPCART 368
```

```
RESULT 12
US-09-144-914-8
Sequence 8, Application US/09144914
GENERAL INFORMATION:
APPLICANT: Duprat, Fabrice
APPLICANT: Lesage, Florian
APPLICANT: Fink, Michel
APPLICANT: Lazdunski, Michel
TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
FILE REFERENCE: 989, 6705CIP
CURRENT APPLICATION NUMBER: US/09/144,914
CURRENT FILING DATE: 1998-09-01
EARLIER APPLICATION NUMBER: 08/749,816
EARLIER FILING DATE: 1996-11-15
EARLIER APPLICATION NUMBER: 60/095,234
```

```
EARLIER FILING DATE: 1998-08-04
EARLIER APPLICATION NUMBER: FR 96/01565
EARLIER FILING DATE: 1996-02-08
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 370
TYPE: PRT
ORGANISM: Murine
FEATURE:
OTHER INFORMATION: TREK-1
US-09-144-914-8
```

```
Query Match      86.9% Score 1824; DB 15; Length 370;
Best Local Similarity 96.5%; Pred. No. 1.3e-175;
Matches 355; Conservative 8; Mismatches 5; Indels 0; Gaps 0;
```

```
OY 1 MAAPDLDPKSAONSKPRLSFTKPTVLASRVESDPTTNVKKMKTSTFLVVLXLI 60
DB 1 MAAPDLDPKSAONSKPRLSFTKPTVLASRVESDPTTNVKKMKTSTFLVVLXLI 60
OY 61 GAVFKALEQPEISORTTIVIOKOTFISQHCVNSTEDELIOQIVAAINAGIPLGNT 120
DB 61 GAVFKALEQPEISORTTIVIOKOTFISQHCVNSTEDELIOQIVAAINAGIPLGNS 120
OY 121 SNOISHMDLSSFFAGVTITIGFNGISPRTEGKIFCIYALLGIPLEGFLAGVGDO 180
DB 121 SNOISHMDLSSFFAGVTITIGFNGISPRTEGKIFCIYALLGIPLEGFLAGVGDO 180
OY 181 LGTFEKGIAKVEDTPIKNNVSQTKIRIISTIFILFGCVLPAVLFKHIEGMSALD 240
DB 181 LGTFEKGIAKVEDTPIKNNVSQTKIRIISTIFILFGCVLPAVLFKHIEGMSALD 240
OY 241 AIYFVYITLTITIGFDYVAGSDIEYLDYKPYVWFMIILGLAYFAVLSMIGDMLRVIS 300
DB 241 AIYFVYITLTITIGFDYVAGSDIEYLDYKPYVWFMIILGLAYFAVLSMIGDMLRVIS 300
OY 301 KTKKEVGEFRAHAAMTANVTAEFKETRRRLSVEIYDKFORATSIKRLSALAGNHNQ 360
DB 301 KTKKEVGEFRAHAAMTANVTAEFKETRRRLSVEIYDKFORATSIKRLSALAGNHNQ 360
OY 361 ELTPCART 368
DB 361 ELTPCART 368
```

```
RESULT 13
US-09-436-265-8
Sequence 8, Application US/09436265
GENERAL INFORMATION:
APPLICANT: REYES, ROBERTO
APPLICANT: DUPRAT, FABRICE
APPLICANT: LESAGE, FLORIAN
APPLICANT: FINK, MICHEL
APPLICANT: SALINAS, MIGUEL
APPLICANT: FARMAN, NICOLETTE
APPLICANT: LAZDUNSKI, MICHEL
TITLE OF INVENTION: NEW FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR
TITLE OF INVENTION: CLONING AND THEIR USE, ESPECIALLY FOR THE SCREENING OF
TITLE OF INVENTION: DRUGS
FILE REFERENCE: 1201-CIP2-00
CURRENT APPLICATION NUMBER: US/09/436,265
CURRENT FILING DATE: 1999-11-08
PRIOR APPLICATION NUMBER: 60/095,234
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 60/107,692
PRIOR FILING DATE: 1996-11-09
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 370
TYPE: PRT
```

11/9/98  
not  
1996

ORGANISM: Murine sp.  
FEATURE:  
OTHER INFORMATION: TREK-1  
US-09-436-265-8

Query Match 86.9% Score 1824; DB 18; Length 370;  
Best Local Similarity 96.3%; Pred. No. 1.3e-175;  
Matches 355; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

1 MAADLLDPKSAONSPRLSFTSTKPTVLASRVSDPTINVMKKKTVSTIFLVVVLII 60  
1 MAADLLDPKSAONSPRLSFTSTKPTVLASRVSDPTINVMKKKTVSTIFLVVVLII 60  
1 MAADLLDPKSAONSPRLSFTSTKPTVLASRVSDPTINVMKKKTVSTIFLVVVLII 60  
61 GATVFKALQEPHEISORTTIVIQOTFISQHCYCNSTELDELIOQIYVAIINAGIIPGNT 120  
61 GATVFKALQEPHEISORTTIVIQOTFISQHCYCNSTELDELIOQIYVAIINAGIIPGNT 120  
61 GATVFKALQEPHEISORTTIVIQOTFISQHCYCNSTELDELIOQIYVAIINAGIIPGNT 120  
61 GATVFKALQEPHEISORTTIVIQOTFISQHCYCNSTELDELIOQIYVAIINAGIIPGNT 120  
121 SNOISHMDLSSFFFACTVTTTIGFNGINSPRTBEGKIFCIITIALGIPLEGFLLAGVGDQ 180  
121 SNOISHMDLSSFFFACTVTTTIGFNGINSPRTBEGKIFCIITIALGIPLEGFLLAGVGDQ 180  
121 SNOISHMDLSSFFFACTVTTTIGFNGINSPRTBEGKIFCIITIALGIPLEGFLLAGVGDQ 180  
181 LGTFEGKIAKVEDPTFKMNVSOIKIRIISTIFLFGCVLFVALPATIEFHIEGMSALD 240  
181 LGTFEGKIAKVEDPTFKMNVSOIKIRIISTIFLFGCVLFVALPATIEFHIEGMSALD 240  
241 AIYFVVTITLTIGFGDVAGSDIEYDFYKPVVFWILVGLAFVAVLSMIGMLRIVS 300  
241 AIYFVVTITLTIGFGDVAGSDIEYDFYKPVVFWILVGLAFVAVLSMIGMLRIVS 300  
241 AIYFVVTITLTIGFGDVAGSDIEYDFYKPVVFWILVGLAFVAVLSMIGMLRIVS 300  
301 KKTREEVEGFRAHAETANVTAEFKETRRRLSVEIYDKFORATSIKRLSAGELAGNHQ 360  
301 KKTREEVEGFRAHAETANVTAEFKETRRRLSVEIYDKFORATSIKRLSAGELAGNHQ 360  
301 KKTREEVEGFRAHAETANVTAEFKETRRRLSVEIYDKFORATSIKRLSAGELAGNHQ 360  
301 KKTREEVEGFRAHAETANVTAEFKETRRRLSVEIYDKFORATSIKRLSAGELAGNHQ 360  
361 ELTPCRRT 368  
361 ELTPCRRT 368

RESULT 14  
PCT-US01-14965-73  
Sequence 73. Application PC/TUS0114965  
GENERAL INFORMATION:  
APPLICANT: Pharmacia & Upjohn Company  
APPLICANT: Robertus, Steven L.  
APPLICANT: Benjamin, Christopher  
APPLICANT: Karnovsky, Alla M.  
APPLICANT: Ruble, Cara L.  
TITLE OF INVENTION: Human Ion Channels  
FILE REFERENCE: 00133.PCT1  
CURRENT APPLICATION NUMBER: PCT/US01/14965  
CURRENT FILING DATE: 2001-05-10  
PRIOR APPLICATION NUMBER: 60/203,305  
PRIOR FILING DATE: 2000-05-10  
PRIOR APPLICATION NUMBER: 60/207,092  
PRIOR FILING DATE: 2000-05-25  
PRIOR APPLICATION NUMBER: 60/206,526  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,033  
PRIOR FILING DATE: 2000-05-25  
PRIOR APPLICATION NUMBER: 60/207,093  
PRIOR FILING DATE: 2000-05-25  
PRIOR APPLICATION NUMBER: 60/216,893  
PRIOR FILING DATE: 2000-07-17  
PRIOR APPLICATION NUMBER: 60/237,873  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: 60/223,245  
PRIOR FILING DATE: 2000-08-04  
NUMBER OF SEQ ID NOS: 88  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 73  
LENGTH: 543  
TYPE: PRT

ORGANISM: Homo sapiens  
PCT-US01-14965-73

Query Match 59.2% Score 1243; DB 18; Length 543;  
Best Local Similarity 62.7%; Pred. No. 1.9e-11; Indels 28; Gaps 6;  
Matches 247; Conservative 54; Mismatches 5; Indels 28; Gaps 6;

2 AAPDLDPKSA-----AONSKPRLSFTSTKPTVLASRVSDPTINVMKKKTVSTI 50  
22 AAAPVQCPKATNQPPAPATPPRLSISRATVVA-FRISQGLQYVMKKKTVYAI 80  
51 FLVVVLIIIGATVFKALQEPHEISORTTIVIQOTFISQHCYCNSTELDELIOQIYVAI 110  
81 FVVVVVVLVLTGVLFRALQEPHEISORTTIVIQOTFISQHCYCNSTELDELIOQIYVAI 140  
111 NAGIIPGNTSNOISHMDLSSFFFACTVTTTIGFNGINSPRTBEGKIFCIITIALGIPLEGFLLAGVGDQ 170  
141 NAGVSPIGNSSSHMDLSSFFFACTVTTTIGFNGINSPRTBEGKIFCIITIALGIPLEGFLLAGVGDQ 200  
171 GELLAGVGDQGTTFEGKIAKVEDPTFKMNVSOIKIRIISTIFLFGCVLFVALPATIEFHIEGMSALD 230  
201 GELLAGVGDQGTTFEGKIAKVEDPTFKMNVSOIKIRIISTIFLFGCVLFVALPATIEFHIEGMSALD 260  
231 KHEGWSALDAIYFVVTITLTIGFGDVAGG-SDIEYDFYKPVVFWILVGLAFVAVLSMIGMLRIVS 289  
261 KYIGWTALESIEYFVVTITLTIGFGDVAGG-SDIEYDFYKPVVFWILVGLAFVAVLSMIGMLRIVS 320  
290 SMIDMLRVISKKTREEVEGFRAHAETANVTAEFKETRRRLSVEIYDKFORATSIKRLSAGELAGNHQ 349  
321 SMIDMLRVISKKTREEVEGFRAHAETANVTAEFKETRRRLSVEIYDKFORATSIKRLSAGELAGNHQ 378  
350 LSAELAGNHQDELTPCRRTLSVNLJNDRDVLPP 383  
379 -SME-----RRRLGDLQRAHSLDMLSP 399

RESULT 15  
US-09-852-386-73  
Sequence 73. Application US/09852386  
GENERAL INFORMATION:  
APPLICANT: Robertus, Steven L.  
APPLICANT: Benjamin, Christopher  
APPLICANT: Karnovsky, Alla M.  
APPLICANT: Ruble, Cara L.  
TITLE OF INVENTION: Human Ion Channels  
FILE REFERENCE: 00133.US1  
CURRENT APPLICATION NUMBER: US/09/852,386  
CURRENT FILING DATE: 2001-05-10  
PRIOR APPLICATION NUMBER: 60/203,305  
PRIOR FILING DATE: 2000-05-10  
PRIOR APPLICATION NUMBER: 60/207,092  
PRIOR FILING DATE: 2000-05-25  
PRIOR APPLICATION NUMBER: 60/206,526  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,033  
PRIOR FILING DATE: 2000-05-25  
PRIOR APPLICATION NUMBER: 60/207,093  
PRIOR FILING DATE: 2000-05-25  
PRIOR APPLICATION NUMBER: 60/216,893  
PRIOR FILING DATE: 2000-07-17  
PRIOR APPLICATION NUMBER: 60/237,873  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: 60/223,245  
PRIOR FILING DATE: 2000-08-04  
NUMBER OF SEQ ID NOS: 88  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 73  
LENGTH: 543  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-852-386-73



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 28, 2001, 16:57:36 ; Search time 28.01 Seconds  
(without alignments)  
302.129 Million cell updates/sec

Title: US-09-503-089a-2  
Perfect score: 2100  
Sequence: 1 MAAPDLDPKSAQNSKPRRL.....LNGLPHCAGEIAVENIK 411

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*

1: /cgn2\_6/prodata/2/1aa/5a\_COMB.pep:\*  
2: /cgn2\_6/prodata/2/1aa/5b\_COMB.pep:\*  
3: /cgn2\_6/prodata/2/1aa/5a\_COMB.pep:\*  
4: /cgn2\_6/prodata/2/1aa/5b\_COMB.pep:\*  
5: /cgn2\_6/prodata/2/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/prodata/2/1aa/backfillsl.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2095	99.8	411	4	US-09-236-080-2
2	2035	96.9	411	4	US-09-236-080-6
3	547	26.0	107	4	US-09-236-080-4
4	379.5	18.1	336	3	US-08-749-816-2
5	291.5	13.9	618	1	US-08-332-312-2
6	221	10.5	336	1	US-08-332-312-4
7	179	8.5	333	3	US-08-749-816-3
8	160.5	7.6	347	3	US-08-749-816-4
9	120	5.7	676	4	US-09-135-021-2
10	103.5	4.9	581	4	US-09-135-021-80
11	99.5	4.7	831	2	US-08-677-734A-11
12	99.5	4.7	834	2	US-08-677-734A-9
13	99.5	4.7	834	2	US-08-677-734A-10
14	97.5	4.6	832	2	US-08-677-734A-12
15	96.5	4.6	1036	2	US-08-720-484A-5
16	96.5	4.6	1036	4	US-08-953-823A-5
17	94.5	4.5	548	3	US-08-903-139B-28
18	94	4.5	535	3	US-08-286-870A-6
19	94	4.5	648	3	US-08-286-870A-4
20	94	4.5	719	3	US-08-286-870A-8
21	93.5	4.5	626	2	US-08-956-242-2
22	93.5	4.5	626	3	US-09-351-215-2
23	93.5	4.5	1159	2	US-08-956-242-13
24	93.5	4.5	1159	3	US-09-351-215-13
25	93.5	4.5	1159	4	US-09-226-012-2
26	93.5	4.5	1159	4	US-09-226-012-4
27	93	4.4	606	3	US-08-620-077B-3

28	92.5	4.4	473	1	US-08-597-236-	Sequence 13, Appl
29	92.5	4.4	473	1	US-08-746-682A	Sequence 13, Appl
30	91.5	4.4	548	3	US-08-903-139B	Sequence 9, Appl
31	91	4.3	888	2	US-08-956-242-1	Sequence 4, Appl
32	91	4.3	888	3	US-09-351-215-6	Sequence 4, Appl
33	90.5	4.3	547	3	US-08-903-139B-	Sequence 7, Appl
34	90.5	4.3	550	4	US-08-637-823B-	Sequence 30, Appl
35	90	4.3	552	3	US-09-111-752-7	Sequence 7, Appl
36	89.5	4.3	1872	6	5386025-6	Sequence 4, Appl
37	88.5	4.2	483	4	US-08-637-823B-4	Sequence 4, Appl
38	88	4.2	482	2	US-08-637-823B-4	Sequence 5, Appl
39	88	4.2	548	2	US-08-676-279-5	Sequence 50, Appl
40	88	4.2	548	3	US-08-903-139B-	Sequence 8, Appl
41	88	4.2	548	4	US-08-637-823B-	Sequence 25, Appl
42	87.5	4.2	436	6	5432081-10	Sequence 32, Appl
43	87.5	4.2	482	4	US-08-637-823B-3	Sequence 32, Appl
44	87.5	4.2	484	4	US-08-637-823B-2	Sequence 2, Appl
45	87	4.1	548	1	US-07-675-211-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1	US-09-236-080-2	Application us/09236080
Sequence 2, Appl	Patent No. 6242217	
GENERAL INFORMATION:		
APPLICANT:	Helen Meadows	
APPLICANT:	Conrad Chapman	
TITLE OF INVENTION:	No. 6242217el Compounds	
FILE REFERENCE:	GP30031	
CURRENT APPLICATION NUMBER:	us/09/236, 080	
CURRENT FILING DATE:	1999-01-25	
NUMBER OF SEQ ID NOS:	6	
SOFTWARE:	FastSeq for Windows Version 3.0	
SEQ ID NO 2		
LENGTH:	411	
TYPE:	PRT	
ORGANISM:	Homo sapiens	
US-09-236-080-2		
Query Match	99.8% Score 2095; Df	Length 411;
Best Local Similarity	99.8% Pred. No. 5e-2.	
Matches 410; Conservative 1; Mismatches		Indels 0; Gaps 0;
QY 1	MAAPDLDPKSAQNSKPRLSFTKPTVLASRVESDPTT	MAAKTVSTFLVVLVLI 60
Db 1	MAAPDLDPKSAQNSKPRLSFTKPTVLASRVESDPTT	MAAKTVSTFLVVLVLI 60
QY 61	GATYFKALBOPHEISORTTIVIOKOTFISOHSCVNSTE	IOOIYAIAINAGIIPRGNT 120
Db 61	GATYFKALBOPHEISORTTIVIOKOTFISOHSCVNSTE	IOOIYAIAINAGIIPRGNT 120
QY 121	SNQSHMDLSSPFACVTITTTIGFGNISPRTEGKIFC	IYALALGILPFLGFLAGVGDQ 180
Db 121	SNQSHMDLSSPFACVTITTTIGFGNISPRTEGKIFC	IYALALGILPFLGFLAGVGDQ 180
QY 181	LGTIFGKIAKVEDTFTIKMNVSOFTKIRIISTIFILEG	CLFVALPAIIFKHIEGMSALD 240
Db 181	LGTIFGKIAKVEDTFTIKMNVSOFTKIRIISTIFILEG	CLFVALPAIIFKHIEGMSALD 240
QY 241	AIYFVITLTITIGGDVAVAGSDIEYIDFKPPVFMILVC	AVFAAVLSMIGWMLVIS 300
Db 241	AIYFVITLTITIGGDVAVAGSDIEYIDFKPPVFMILVC	AVFAAVLSMIGWMLVIS 300
QY 301	KKTKEEYGEFRRAHAEMTANTAFKETRRLSVEIDK	FMATSIKRLSAELAGNHQ 360
Db 301	KKTKEEYGEFRRAHAEMTANTAFKETRRLSVEIDK	FMATSIKRLSAELAGNHQ 360
QY 361	ELAPCRFTLSVNLITNERDVLPIILKTESIYLANGLPH	RCJAVIENIK 411
Db 361	ELAPCRFTLSVNLITNERDVLPIILKTESIYLANGLPH	RCJAVIENIK 411

Db 361 ELTPCRRRTLSVNHLSERDVLPPLLKTESITYLNGLPHPGAGEIATVENIK 411

## RESULT 2

US-09-236-080-6  
Sequence 6, Application US/09236080  
Patent No. 6242217  
GENERAL INFORMATION:  
APPLICANT: Helen Meadows  
APPLICANT: Conrad Chapman  
TITLE OF INVENTION: No. 6242217el Compounds  
FILE REFERENCE: GP30031  
CURRENT APPLICATION NUMBER: US/09/236,080  
CURRENT FILING DATE: 1999-01-25  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 6  
LENGTH: 411  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-236-080-6

Query Match 96.9%; Score 2035; DB 4; Length 411;  
Best Local Similarity 95.9%; Pred. No. 6.9e-200;  
Matches 394; Conservative 12; Mismatches 5; Indels 0; Gaps 0;

OY 1 MAAPDLDPKSAONSKPRLSFSKPTVLASRYESDFTIIVMKTKVSTFLVVLVLI 60  
Db 1 MAAPDLDPKSAONSKPRLSFSKPTVLASRYESDFTIIVMKTKVSTFLVVLVLI 60  
OY 61 GATVFKALEOPHEISORTTIVIOKOTFISOHSCVNSTELDELIOQIVAAINAGIIPLANT 120  
Db 61 GAATVFKALEOPHEISORTTIVIOKOTFISOHSCVNSTELDELIOQIVAAINAGIIPLANS 120  
OY 121 SNOISHMDDLSSFFPACTVITTTGFGNISPTREBGIKFCIIVALLGIFLFGFLAGVGDQ 180  
Db 121 SNOVSHMDLSSFFPACTVITTTGFGNISPTREBGIKFCIIVALLGIFLFGFLAGVGDQ 180  
OY 181 LGTFGKGIAKVEDTFIKMNVISOTKIRIITITIFILFGCVLPAALPPIIKHIEGMSALD 240  
Db 181 LGTFGKGIAKVEDTFIKMNVISOTKIRIITITIFILFGCVLPAALPPIIKHIEGMSALD 240  
OY 241 AIYFVVITLTIGFGDYVAGSDIEYDFKPYVWFILVGLAYFAVLMSIDWLRVIS 300  
Db 241 AIYFVVITLTIGFGDYVAGSDIEYDFKPYVWFILVGLAYFAVLMSIDWLRVIS 300  
OY 301 KTKKEVGEFRRAAEVTAETVTAETKTRRLSVEIYDFQKATSTIKRISAEIAGNHQ 360  
Db 301 KTKKEVGEFRRAAEVTAETVTAETKTRRLSVEIYDFQKATSTIKRISAEIAGNHQ 360  
OY 361 ELTPCRRRTLSVNHLSERDVLPPLLKTESITYLNGLPHPGAGEIATVENIK 411  
Db 361 ELTPCRRRTLSVNHLSERDVLPPLLKTESITYLNGLPHPGAGEIATVENIK 411

## RESULT 3

US-09-236-080-4  
Sequence 4, Application US/09236080  
Patent No. 6242217  
GENERAL INFORMATION:  
APPLICANT: Helen Meadows  
APPLICANT: Conrad Chapman  
TITLE OF INVENTION: No. 6242217el Compounds  
FILE REFERENCE: GP30031  
CURRENT APPLICATION NUMBER: US/09/236,080  
CURRENT FILING DATE: 1999-01-25  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 4  
LENGTH: 107  
TYPE: PRT  
ORGANISM: Homo sapiens

US-09-236-080-4

Query Match 26.0%; Score 547; DB 1; Length 107;  
Best Local Similarity 98.1%; Pred. No. 1.5e-8;  
Matches 105; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 119 NTSNOISHMDDLSSFFPACTVITTTGFGNISPTREBGIKFCIIVALLGIFLFGFLAGV 178  
Db 1 NTSNOISHMDDLSSFFPACTVITTTGFGNISPTREBGIKFCIIVALLGIFLFGFLAGV 178  
OY 179 DQGTIFGKGIAKVEDTFIKMNVISOTKIRIITITIFILFGCVLPAALPPIIKHIEGMSALD 225  
Db 61 DQGTIFGKGIAKVEDTFIKMNVISOTKIRIITITIFILFGCVLPAALPPIIKHIEGMSALD 225

## RESULT 4

US-08-749-816-2  
Sequence 2, Application US/08749816  
Patent No. 6013470  
GENERAL INFORMATION:  
APPLICANT: Lesage, Florian  
APPLICANT: Guillemaire, Eric  
APPLICANT: Fink, Michel  
APPLICANT: Duprat, Fabrice  
APPLICANT: Lazdunski, Michel  
APPLICANT: Romey, Georges  
APPLICANT: Barhanin, Jacques

TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS,  
TITLE OF INVENTION: THEIR CLONING AND THEIR USE ESPECIALLY FOR THE SCREENING  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSER: WEISER & ASSOCIATES  
STREET: 230 South Fifteenth Street, Suite 300  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19102

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version 4.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/749,816  
FILING DATE: 15-NOV-1996  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Weiser, Gerard J.  
REGISTRATION NUMBER: 19,763  
REFERENCE/DOCKET NUMBER: 989,6351P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-875-8383  
TELEFAX: 215-875-8394

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 336 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-749-816-2

Query Match 18.1%; Score 379.5; DB 1; Length 336;  
Best Local Similarity 32.5%; Pred. No. 1.1e-3;  
Matches 90; Conservative 62; Mismatches 106; Indels 17; Gaps 9;

OY 51 FLVAV--VYLIIIGATVFKALEOPHEISORTTIVIOKOTFISJHSCVNSTELDELIOQIVAA 108  
Db 25 FLVAV--VYLIIIGATVFKALEOPHEISORTTIVIOKOTFISJHSCVNSTELDELIOQIVAA 108  
OY 109 AINAGIIPLANTSGNOSISHMDDLSSFFPACTVITTTGFGNISPTREBGIKFCIIVALLGIP 168



DB 85 ASNGSVLSVSNASGN-NMWDFTSALFFASTVLTSTTGGHTVPLSDGKAFCLITSVIGIP 143  
QY 169 LFGCLAGVGGDGLTIGKGIKAKVEDFEIKWNVOTKIRIISTII--FILEGCVLFVALP 226  
DB 144 FTLLFLAVRVRITVHYTR--RPVLYFEIRKRGFSKQVAVIAHVALLGVTVCSEFFI--P 199  
QY 227 AIFKHIE-GMSALDAIYFVYITLTITGFDGVAG-GSDIEYLDYFKPVVFWIIVGLAY 284  
DB 200 AAFSVLEDDWNLFESEFYCFISLSTIGLDGVPEGVNQKFRLELYKIGICVYLLGLIA 259  
QY 285 FAVLSTHGMRLVYSK-----KTKEVGEFRHAAE 316  
DB 260 MLVYLETFC-LHELKFRKMYVKKDKDEDQVHIIE 295

RESULT 5  
US-08-332-312-2  
Sequence 2, Application US/08332312  
Patent No. 5559026

GENERAL INFORMATION:  
APPLICANT: Price, Laura A.  
TITLE OF INVENTION: Functional Expression of a Drosophila  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: American Cyanamid Company  
STREET: One Cyanamid Plaza  
CITY: Wayne  
STATE: New Jersey  
COUNTRY: US  
ZIP: 07470-8426

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/332.312  
FILING DATE:

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Harrington, James J.  
REGISTRATION NUMBER: P-38,711  
REFERENCE/DOCKET NUMBER: 32,421  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-831-3246  
TELEFAX: 201-831-3305

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 618 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-332-312-2

Query Match 13.9%; Score 291.5; DB 1; Length 618;  
Best Local Similarity 27.8%; Pred. No. 2.8e-21;

Matches 88; Conservative 64; Mismatches 123; Indels 41; Gaps 13;

QY 50 IFVLVVLVLLIGATVFNALBEPHE---ISORTIVIVKQRFISQHSOVNSTELDELIOQ 105  
DB 9 LLIIYISLIMGALYIHHIEGEEKISRAEQRKQAIANELELLDGNKTTTODELIQR 68  
QY 106 IVAAIMAGIPLGNISQISHWLGSSEFFAGVYITITGFGNISPRTEGKIFCIYALL 165  
DB 69 ISDCKRVTLPPTYDDPPTWTFYHAFVAFVCSVYGYNISPTFPAGMIMIAVSVI 128  
QY 166 GIPLEGLIAGVGGDGLTIGKGIKAKVEDFEIKWNV-----OTKIRIISTIIIFILF-G 218  
DB 129 GIPVNGIIFAG---LGEYFGRTFEAIVRYRYKRYKMSDMHYVPPOLGLITVVIALIPG 184

QY 219 CVLFLVALPAI---IFKHIEGMSALDAIYFVYITLTITGFGHVA-----GSDIE 265  
DB 185 IALFLVLPVCVGHLLREL-GLSSI-SLYSVYTTTIGFGI'V'VPTFGANQKREGGMFV 242  
QY 266 YLDYFKPVVFWIIVGLAYFAVYLSMIGDMLRVYSK-~~Y~~KEVGEFRHAAEWANV 321  
DB 243 YQIVV--IWMF--IFSLGYLVMIMFTTRIGQ--SKRL--GLSSNLKATONRIMSGV 296  
QY 322 TAEFKETRRRLSEIY 337  
DB 297 TKDGYLRRLN-ELY 311

RESULT 6  
US-08-332-312-4  
Sequence 4, Application US/08332312  
Patent No. 5559026

GENERAL INFORMATION:  
APPLICANT: Price, Laura A.  
TITLE OF INVENTION: Functional Expression of a Drosophila  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: American Cyanamid Company  
STREET: One Cyanamid Plaza  
CITY: Wayne  
STATE: New Jersey  
COUNTRY: US  
ZIP: 07470-8426

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/332.312  
FILING DATE:

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Harrington, James J.  
REGISTRATION NUMBER: P-38,711  
REFERENCE/DOCKET NUMBER: 32,421  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-831-3246  
TELEFAX: 201-831-3305

INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 336 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-332-312-4

Query Match 10.5%; Score 221; DB 1; Length 336;  
Best Local Similarity 26.2%; Pred. No. 1.8e-11;

Matches 59; Conservative 37; Mismatches 17; Indels 52; Gaps 6;

QY 120 TSNQISH-----WDLGSEFFAGVYITITGFGNISPRTH--KIFCIYALLGIPLEGFL 173  
DB 15 TSNEVKNAATEWTFSSIFFAVTVTTIGYGNPVPVNTINIRIMCLIFSLGIPL--T 71  
QY 174 LAGVGDLGTIFGKGIKAKVEDFTIK-----WNSQT 204  
DB 72 LVTLADLAGKFLSHLWLVGNYLKLYLLISRRRKERRI--CEHSHGSHDMNTEER 131  
QY 205 KIRIISTIIIFLCVFLVALPAIIFKHIEGMSALDAIY-VITLTIGFDGVAGGSDI 264  
DB 132 RI-----FAVLVALIIVYTAGVGLMSKLEPWSFTSTYR-ITIMTVGFGDMLPRDGY 187  
QY 265 EYLDL-----YKPVVFWIIVGLAYFAVYLSMIG-MLRVY 299



QY 216 LFGCVLPAALIAIEKHEGMSALDAIYFVITLTITIGFDYVAGSGDIEYDEKPYVM 275  
 Db 208 LLCSITLSSSALFSSSIENTSYLSSVFGITITWELIGDITVPTN-----LWV 256  
 QY 276 F 276  
 Db 257 F 257

## RESULT 9

US-09-135-021-2  
 ; Sequence 2, Application US/09135021A  
 ; Patent No. 6150104  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Splawski, Igor  
 ; APPLICANT: Keating, Mark T.  
 ; TITLE OF INVENTION: A HOMOOZIGOUS MUTATION IN KYLOT1 WHICH CAUSES JERVELL  
 ; FILE REFERENCE: 2323-128  
 ; CURRENT APPLICATION NUMBER: US/09/135,021A  
 ; EARLIER FILING DATE: 1998-08-17  
 ; EARLIER APPLICATION NUMBER: 08/874,655  
 ; EARLIER FILING DATE: 1997-06-13  
 ; EARLIER APPLICATION NUMBER: 60/094,477  
 ; EARLIER FILING DATE: 1998-07-29  
 ; NUMBER OF SEQ ID NOS: 80  
 ; SOFTWARE: Patentln Ver. 2.0  
 ; SEQ ID NO 2  
 ; LENGTH: 676  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-135-021-2

Query Match 5.78; Score 120; DB 4; Length 676;  
 Best Local Similarity 19.48; Pred. No. 0.0011;  
 Matches 90; Conservative 70; Mismatches 137; Indels 166; Gaps 24;

QY 2 AAPDL---LQKSAONSKPRLS-FSTRPYVLASRVESDTINMK-----KTV---STI 50  
 Db 71 AAPVYASDLGRPPV-SIDRPVSTYSTRPYLATRHOGARYNLEPRTGKCKVYHFAV 129  
 QY 51 FLVVVLLIIGATVFKALEOPHEISORTTIVIOKOTFISCHSVNSTELDELIOIYVAI 110  
 Db 130 FLIYVLCIF--SVLSTIEQYALATGLTFLM-----EIVLYV 165  
 QY 111 NAGIIPGANTSNQISHMDLSSFFPAG-----TVITTTIGFN 147  
 Db 166 FFG-----TEYVYRLMSAGCRSKYVGLMGRLEAPRKPISTIDLIYVAVSMVLCVG--- 216  
 QY 148 ISPTREGKICICIIYALIGLPLFGFL-LAGVGDGLTIFGKIAKVEDTFIKMNVSOIKI 206  
 Db 217 -----SKQVPA-TSAIRGIRFLQILRLMHVDRGGT-----W----- 248  
 QY 207 RIISTITFI--LFGCVLPAALIAIEK-----HIEGMSALDAIYFVI 247  
 Db 249 RLDSVVEIHRQELITLTYIGFLIFSSFYVLAEKDAVNESGVERGSVAADLMMGV 308  
 QY 248 TLITIGREDIYVAGSDIEYLDYKPYVWF-----MLVGLAFYAAVLSMIGDM--LRV 298  
 Db 309 TTTTIGYGDVY-----PQTVWGKTIASCFVSFAISFPALPAGILGSGFALKV 355  
 QY 299 ISKTKKEVGE-----FRAHAAE-----WTANYTAERKETRRRLSYEIKYKF 340  
 Db 356 QOKOROKHFNQOIRPAASLIOTAMRCYAAENPDSSTWKIYIR---KAPRSHLISPSKRP 412  
 QY 341 QRAFSIKRRLSAGLAGNHQELTPCQRTLSVNHLLTNERDVLPP 383  
 Db 413 KKSYYVKKK---KFLDKDNGVTGPEKKMLVPHITCD---PP 448

RESULT 10

US-09-135-021-80  
 ; Sequence 80, Application US/09135021A  
 ; Patent No. 6150104  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Splawski, Igor  
 ; APPLICANT: Keating, Mark T.  
 ; TITLE OF INVENTION: A HOMOOZIGOUS MUTATION IN KYLOT1 WHICH CAUSES JERVELL  
 ; FILE REFERENCE: 2323-128  
 ; CURRENT APPLICATION NUMBER: US/09/135,021A  
 ; EARLIER FILING DATE: 1998-08-17  
 ; EARLIER APPLICATION NUMBER: 08/874,655  
 ; EARLIER FILING DATE: 1997-06-13  
 ; EARLIER APPLICATION NUMBER: 60/094,477  
 ; EARLIER FILING DATE: 1998-07-29  
 ; NUMBER OF SEQ ID NOS: 80  
 ; SOFTWARE: Patentln Ver. 2.0  
 ; SEQ ID NO 80  
 ; LENGTH: 581  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-135-021-80

Query Match 4.98; Score 103.5; DB 4; Length 581;  
 Best Local Similarity 18.48; Pred. No. 0.043;  
 Matches 76; Conservative 62; Mismatches 118; Indels 157; Gaps 20;

QY 44 WKTV---STIFLVVLLIIGATVFKALEOPHEISORTTIVIOKOTFISCHSVNSTELD 100  
 Db 25 WKCFVYHFAVFLIYVLCIF--SVLSTIEQYALATGLTFLM-----EIVLYV 64  
 QY 101 ELIOQVIAINAGIIPGANTSNQISHMDLSSFFPAG-----KTV---STI 137  
 Db 65 -----EIVLYVFPG-----TEYVYRLMSAGCRSKYVGLMGRLEAPRKPISTIDLIYVAVS 114  
 QY 138 TVITTTIGFNISPTREGKICICIIYALIGLPLFGFL-LAGVGDGLTIFGKIAKVEDTF 196  
 Db 115 MVVLCVG-----SKQVPA-TSAIRGIRFLQILRLMHVDRGGT-----W----- 152  
 QY 197 IKMNVSOIKIISTITFI--LFGCVLPAALIAIEK-----HIEGMS 237  
 Db 153 -W-----RLDSVVEIHRQELITLTYIGFLIFSSFYVLAEKDAVNESGVERGS 203  
 QY 238 ALDAIYFVITLTITIGREDIYVAGSDIEYLDYKPYVWF-----MLVGLAFYAAVLS 290  
 Db 204 YADALMGVYVTTITIGDVKY-----PQTVWGKTIASCFVSFAISFPALPAG 250  
 QY 291 MIGDM--LRVYSKTKKEVGE-----FRAHAAE-----WTANYTAERKETRR 330  
 Db 251 ILGSGFLAKVQOKOROKHFNQOIRPAASLIOTAMRCYAAENPDSSTWKIYIR---KAPR 307  
 QY 331 RLSEYIDKFORAISIKRRLSAGLAGNHQELTPCQRTLSVNHLLTNERDVLPP 383  
 Db 308 HTLSPSPKRPKSYVKKK---KFLDKDNGVTGPEKKMLVPHITCD---PP 353

## RESULT 11

US-08-677-734A-11  
 ; Sequence 11, Application US/08677734A  
 ; Patent No. 5871919  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Brant, Steven R.  
 ; APPLICANT: Yun, Chris C.H.  
 ; APPLICANT: Donowitz, Mark  
 ; APPLICANT: Tse, Chung-Ming  
 ; TITLE OF INVENTION: Cloning, Tissue Distribution, and  
 ; TITLE OF INVENTION: Functional Analysis Of the Human Na+/H+ Exchanger Isoform,  
 ; NUMBER OF SEQUENCES: 12  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
 ; ADDRESSEE: Dunner

RESULT 12  
US-08-677-734A-9  
Sequence 9, Application US/08677734A  
Patent No. 5819199  
GENERAL INFORMATION:  
APPLICANT: Branlt, Steven R.  
APPLICANT: Iun, Chris C. H.  
APPLICANT: Donowitz, Mark  
APPLICANT: Ise, Chung-Ming

RESULT 13  
US-08-677-734A-10  
; Sequence 10, Application US/08677734A  
; Patent No. 5871919  
; GENERAL INFORMATION:  
; APPLICANT: Brant, Steven R.

APPLICANT: Yun, Chris C.H.  
APPLICANT: Donowitz, Mark  
APPLICANT: Tse, Chung-Ming  
TITLE OF INVENTION: Cloning, Tissue Distribution, and  
TITLE OF INVENTION: Functional Analysis Of The Human Na+/H+ Exchanger Isoform,  
TITLE OF INVENTION: NHE3.  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESSEE: Dunner  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/677,734A  
FILING DATE: 10-JUL-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Fordis, Jean B.  
REGISTRATION NUMBER: 32,984  
REFERENCE/DOCKET NUMBER: 05387.0043-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 408-4000  
TELEFAX: (202) 408-4400  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 834 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-677-734A-10

Query Match 4.7% Score 99.5; DB 2; Length 834;  
Best Local Similarity 20.4%; Pred. No. 0.19;  
Matches 73; Conservative 64; Mismatches 93; Indels 127; Gaps 22;  
QY 43 KWKTVSTIFLVVLYLIGATVFKALQPHIEISRTIVIOKOTFISOHSCVNSTEDEL 102  
DB 48 EMAHVODPY-VIALMILVASLAKIGFHLSHKV--TSVPESALLI----- 89  
QY 103 IQQIVAAINAGIIPLGNTSNOISHMDGSSFF-----AGTVI-TTIGFNGISPR 151  
DB 90 ---VLGVLGGIV---WAADHIASFTLTPVFFFYLLPPIVLDAGYFMPNRLFFGNL--- 140  
QY 152 TEGGKIFCIYALL-----GIPLEGFLAG-VGD-OLG---TIFGKIAKVEDTF 196  
DB 141 ---GTI--LLYAVGVVMAATGTLISYGVELSGLMGDLQIGLDFLLGSLMAAVD--- 192  
QY 197 IKMWSTFKIRIISTIFILFCGVLPALPAITFKHIEGSAL-DALYFVITITTTGFG 255  
DB 193 ---PAAVLAVEEVHNEVLEFT---IYF---GESLNDADVAVLYXN---FE 232  
QY 256 DYVA-GGSDIEYIDFYKPVVWFNI-----LVGLAYFAAVLSMIGD---LRVI----- 299  
DB 233 SFVALGSDNTGVDYCVAGIYSFVYSLGGTLGVV-FAFLISLVTRRTKRIIEPGFVF 291  
QY 300 -----SKTRKEVEGFRAHAAEMTANYAEKET 328  
DB 292 IISYLSITSEMLSAIIAIFCGICCKYKVNANISEQSATIVRYTMKMLASSAET 348

RESULT 14  
US-08-677-734A-12  
; Sequence 12, Application US/08677734A

Patent No. 5871919  
GENERAL INFORMATION:  
APPLICANT: Brant, Steven R.  
APPLICANT: Yun, Chris C.H.  
APPLICANT: Donowitz, Mark  
APPLICANT: Tse, Chung-Ming  
TITLE OF INVENTION: Cloning, Tissue Distribution, and  
TITLE OF INVENTION: Functional Analysis Of The Human Na+/H+ Exchanger Isoform,  
TITLE OF INVENTION: NHE3.  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESSEE: Dunner  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/677,734A  
FILING DATE: 10-JUL-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Fordis, Jean B.  
REGISTRATION NUMBER: 32,984  
REFERENCE/DOCKET NUMBER: 05387.0043-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 408-4400  
TELEFAX: (202) 408-4400  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 832 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-677-734A-12

Query Match 4.6% Score 97.5; DB 2; Length 832;  
Best Local Similarity 19.7%; Pred. No. 0.31;  
Matches 73; Conservative 57; Mismatches 93; Indels 147; Gaps 19;  
QY 39 INWKWKTVSTIFLVVLYLIGATVFKALQPHIEISQ-VIOKOTFISOHSCVNSTE 98  
DB 43 IYFKRMHVODPYIIALMVLV--ASLAKIV---FHLSHKVT--VPESALL----- 87  
QY 99 LDELIOIVAAINAGIIPLGNTSNOISHMDGSSFF-----AGTVI-TTIGFNG 147  
DB 88 ---IVGLVGGIVL---AADHIASFTLTPVFFFYLLPPIVLDAGYFMPNRLFFSN 138  
QY 148 ISPTGEGKIFCIYALL-----GIPLEGFLAGVGVGDLGTINGKIAKVEDFIK 198  
DB 139 L-----GSI--LLYAVGVVMAATGTLISYGVLSGI----- 169  
QY 199 MNWSTFKIRIISTIFILFCGVLPALPA-----LIFKHIEGSALD----- 240  
DB 170 ---MELKIGLID---FILFSLIAVDPVAVLANFERYV---VLFITVFGESLNDADV 224  
QY 241 AIYFVITITTTGFGDYVAGSDIEYIDFYKPVVWFNI-----LVGLAYFAAVLSMIGD 294  
DB 225 VLYNVFQSFVTLG-GDKVTG---VDYCVAGIYSFVYSLGGTLGVV-FAFLISLVTR 276  
QY 295 W---LRVI-----SKTRKEVEGFRAHAAEM 317  
DB 277 FTKHVRVIEPGFVFIIISYLSITSEMLSLSIIAIFCGI-KYVKNANISEQSATIVRY 336  
QY 318 TANYAEKET 328





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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 28, 2001, 16:34:15 ; Search time 47.95 Seconds

(Without alignments)  
519.634 Million cell updates/sec

Title: US-09-503-089a-2

Perfect score: 2100

Sequence: 1 MAAPDLDPKSAQNSKPRL.....LNGLTPHCGEEIAVENIK 411

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /SIDSR/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
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21: /SIDSR/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SIDSR/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results, predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2095	99.8	411	20	AA134133 Human potassium ch
2	2095	99.8	411	20	AA128496 h-TREK1 polypeptid
3	2095	99.8	411	22	AA150044 Human TREK_Homo
4	2035	96.9	411	20	AA128497 Mouse h-TREK1 poly
5	1833	87.3	370	20	AA130648 A mechanically sen
6	803	38.2	393	21	AA194425 Human h-TRAAK poly
7	803	38.2	393	21	AA194426 Human h-TRAAK poly
8	776.5	37.0	398	20	AA130647 A mechanically sen
9	547	26.0	107	20	AA128498 Partial h-TREK1 po
10	427	20.3	489	21	AA190356 Human TWIK-2 prote
11	427	20.3	499	21	AA179675 Human potassium ch

12	427	20.3	499	21	AA194875 Human protein clon
13	391	18.6	332	21	AA190354 Human TWIK-3 prote
14	382	18.2	361	22	AA131805 Amino acid sequenc
15	379.5	18.1	336	18	AA123397 TWIK-1 potassium c
16	379.5	18.1	336	21	AA179673 Human potassium ch
17	363	17.3	394	21	AA179674 Human potassium ch
18	363	17.3	394	21	AA187291 Human signal pepti
19	349.5	16.6	374	21	AA181807 Amino acid sequenc
20	349.5	16.6	374	21	AA181807 Amino acid sequenc
21	348	16.6	374	21	AA181807 Amino acid sequenc
22	348	16.6	374	21	AA181807 Amino acid sequenc
23	348	16.6	374	21	AA181807 Amino acid sequenc
24	348	16.6	374	21	AA181807 Amino acid sequenc
25	348	16.6	374	21	AA181807 Amino acid sequenc
26	337	16.0	405	21	AA195230 Mouse potassium ch
27	309.5	14.7	408	22	AA131804 Amino acid sequenc
28	291.5	13.9	618	17	AA197984 DMORF1 potassium c
29	261.5	12.5	395	22	AA131801 Amino acid sequenc
30	221.5	10.5	730	22	AA131800 Amino acid sequenc
31	221	10.5	336	17	AA197986 F22b7.7 potassium
32	209	10.0	995	22	AA131799 Amino acid sequenc
33	179	8.5	383	21	AA179677 Caenorhabditis ele
34	166.5	7.9	1153	22	AA131802 Amino acid sequenc
35	160.5	7.6	347	21	AA179676 Caenorhabditis ele
36	153.5	7.3	197	20	AA134126 Human potassium ch
37	147.5	7.0	316	21	AA134160 Arabidopsis thalia
38	147.5	7.0	316	21	AA134160 Arabidopsis thalia
39	147.5	7.0	408	21	AA134159 Arabidopsis thalia
40	147.5	7.0	408	21	AA134159 Arabidopsis thalia
41	140.5	6.7	399	21	AA141831 Arabidopsis thalia
42	140.5	6.7	424	21	AA141830 Arabidopsis thalia
43	140.5	6.7	424	21	AA141829 Arabidopsis thalia
44	139.5	6.6	248	21	AA141611 Arabidopsis thalia
45	139.5	6.6	248	21	AA140371 Arabidopsis thalia

#### ALIGNMENTS

RESULT 1	AA134133	standard: Protein: 411 AA.
ID	AA134133	
AC	AA134133	
DT	30-NOV-1999	(first entry)
XX		
DE	Human potassium channel K+Hnov59.	
XX		
KM	Potassium channel; ataxia; arrhythmia; epilepsy; Bartter's syndrome;	
KM	cardiovascular disorder; CNS disorder; renal disorder.	
XX		
OS	Homo sapiens.	
XX		
PN	WO943696-A1.	
PD	02-SEP-1999.	
XX		
PF	22-FEB-1999;	99WO-US03826.
XX		
PR	19-JAN-1999;	99US-0116448.
PR	25-FEB-1998;	98US-0076687.
PR	07-AUG-1998;	98US-0095836.
XX		
PA	(AXIS-) AXIS PHARM INC.	
PI	Curran ME, Hu P, Miller AP, Rutter M, Wang J;	
XX		
DR	WPI; 1999-527591/44.	
XX	N-PSDB; AA121915.	
PT	New nucleic acids encoding mammalian K+Hnov potassium channel	
PT	proteins, useful for the diagnosis and treatment of episodic ataxia	

PT with myokymia, cardiac arrhythmia, epilepsy and Bartter's syndrome  
 XX  
 PS Claim 3; Page 104-105; 112pp: English.  
 XX

CC This sequence represents the human K+hov59 potassium channel.  
 CC K+hov proteins have a high degree of homology to known potassium  
 CC channels and may be alpha subunits, which form the functional channel,  
 CC or accessory subunits that act to modulate the channel activity. K+hov59  
 CC is a 4 transmembrane domain, 2 pore domain potassium channel. The gene  
 CC is located on chromosome 19, determined via PCR chromosome  
 CC localisation using primers AA211939 and AA211940. K+hov CDNAS  
 CC were isolated by extension of expressed sequence tags (ESTs) which were  
 CC related but not identical to known human potassium channels. Potential  
 CC polymorphisms detected as sequence variants between multiple  
 CC independent clones. Potassium channels have critical roles in various  
 CC cell types and biochemical pathways. Defective potassium channels are  
 CC known to cause four human diseases: episodic ataxia with myokymia;  
 CC cardiac arrhythmia (long QT syndrome); epilepsy; and Bartter's syndrome.  
 CC As potassium channels are critical components of virtually all cells,  
 CC it is likely that abnormal potassium channels are also implicated in  
 CC certain renal, cardiovascular and central nervous system (CNS)  
 CC disorders. Nucleotides encoding K+hov proteins may be used for  
 CC identifying homologous or related proteins and the DNA sequences encoding  
 CC them. They may be used to produce compositions that modulate the  
 CC expression and function of the K+hov protein and in studying the  
 CC biochemical pathways associated with it. They may also be used for the  
 CC recombinant production of K+hov protein in fermentation cultures.  
 CC Additionally, such nucleotides may be used in gene therapy protocols for  
 CC the treatment of diseases associated with abnormal potassium channels.  
 CC  
 XX  
 XX  
 S0 Sequence 411 AA:

Query Match 99.8%; Score 2095; DB 20: Length 411;  
 Best Local Similarity 99.8%; Pred. No. 1.9e-209;  
 Matches 410; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESPTTINMKKVTSTFLVVLII 60  
 DB 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESPTTINMKKVTSTFLVVLII 60  
 QY 61 GATVFALAEQPHIEISQRTTIVIOKOFIISOHSCVNSTDELIOQIVAINAGIPLGNT 120  
 DB 61 GATVFALAEQPHIEISQRTTIVIOKOFIISOHSCVNSTDELIOQIVAINAGIPLGNT 120  
 QY 61 GATVFALAEQPHIEISQRTTIVIOKOFIISOHSCVNSTDELIOQIVAINAGIPLGNT 120  
 DB 61 GATVFALAEQPHIEISQRTTIVIOKOFIISOHSCVNSTDELIOQIVAINAGIPLGNT 120  
 QY 121 SNOISHMDGSSFFFGTGTITGFGNISPRTEGKRFCTIVALLGPIPLAGVGO 180  
 DB 121 SNOISHMDGSSFFFGTGTITGFGNISPRTEGKRFCTIVALLGPIPLAGVGO 180  
 QY 121 SNOISHMDGSSFFFGTGTITGFGNISPRTEGKRFCTIVALLGPIPLAGVGO 180  
 DB 121 SNOISHMDGSSFFFGTGTITGFGNISPRTEGKRFCTIVALLGPIPLAGVGO 180  
 QY 181 LGTIFGKGLAKVEDTFIKMNSQTKIRIISTIIIFLFGCVLFVALPAIIFKHIEGMSALD 240  
 DB 181 LGTIFGKGLAKVEDTFIKMNSQTKIRIISTIIIFLFGCVLFVALPAIIFKHIEGMSALD 240  
 QY 241 AITFVYITLTITGFGDYVAGSDIEYLDKPPVWMWIIWGLAVFAVLSMIGDWLRVIS 300  
 DB 241 AITFVYITLTITGFGDYVAGSDIEYLDKPPVWMWIIWGLAVFAVLSMIGDWLRVIS 300  
 QY 241 AITFVYITLTITGFGDYVAGSDIEYLDKPPVWMWIIWGLAVFAVLSMIGDWLRVIS 300  
 DB 241 AITFVYITLTITGFGDYVAGSDIEYLDKPPVWMWIIWGLAVFAVLSMIGDWLRVIS 300  
 QY 301 KKTKEEVEGERAAAEWTAETAEFEKTRRRRLSVEIYDKFORATSIKRLSAELAGNHQ 360  
 DB 301 KKTKEEVEGERAAAEWTAETAEFEKTRRRRLSVEIYDKFORATSIKRLSAELAGNHQ 360  
 QY 301 KKTKEEVEGERAAAEWTAETAEFEKTRRRRLSVEIYDKFORATSIKRLSAELAGNHQ 360  
 DB 301 KKTKEEVEGERAAAEWTAETAEFEKTRRRRLSVEIYDKFORATSIKRLSAELAGNHQ 360  
 QY 361 ELTPCRRITLSVNHLTNERDVLPLPLKTESIYINGLTPHCAGEEIAVENIK 411  
 DB 361 ELTPCRRITLSVNHLTNERDVLPLPLKTESIYINGLTPHCAGEEIAVENIK 411

RESULT 2  
 AA28496  
 ID AA28496 standard; Protein; 411 AA.  
 XX  
 AC AA28496;  
 XX  
 DT 12-OCT-1999 (first entry)

XX h-TREK1 polypeptide.  
 DE  
 XX h-TREK1: two pore potassium channel; inflamm. v. nry disease;  
 KW chromosome 1q32.  
 XX  
 XX Homo sapiens.  
 OS  
 PN MO9937762-A1.  
 XX  
 XX 29-JUL-1999.  
 PD  
 XX 02-DEC-1998; 98WO-EP07805.  
 PF  
 XX 09-OCT-1998; 98GB-0022135.  
 PR 27-JAN-1998; 98BP-0300570.  
 XX  
 XX (SMK ) SMITHKLINE BEECHAM PLC.  
 PA  
 XX Chapman CG, Meadows HJ;  
 PI  
 XX WPI: 1999-469126/39.  
 DR N-PSDB: AA200039.  
 DR  
 XX  
 XX New two pore potassium channel used for, e.g. treatment of cancer,  
 PT pulmonary, cardiovascular and inflammatory diseases  
 XX  
 PS Claim 3; Page 24; 44pp: English.

CC This sequence is the h-TREK1 polypeptide, encoded by the h-TREK1  
 CC polynucleotide AA200039. h-TREK1 is a two pore potassium channel, and  
 CC the gene maps to human chromosome 1q32, between the markers D1937 and  
 CC W15105. The polynucleotide sequence of h-TREK1 can be used to diagnose a  
 CC disease or susceptibility to a disease related to expression or activity  
 CC of h-TREK1 polypeptides. The methods of diagnosis may be used in the  
 CC treatment of diseases including cancer, pulmonary, cardiovascular, and  
 CC inflammatory diseases, pain, psychiatric disorders including depression  
 CC and schizophrenia, neurodegenerative diseases including Alzheimer's,  
 CC stroke, and head trauma and neurological disorders including migraine.

S0 Sequence 411 AA:

Query Match 99.8%; Score 2095; DB 20: Length 411;  
 Best Local Similarity 99.8%; Pred. No. 1.9e-209;  
 Matches 410; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESPTTINMKKVTSTFLVVLII 60  
 DB 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESPTTINMKKVTSTFLVVLII 60  
 QY 61 GATVFALAEQPHIEISQRTTIVIOKOFIISOHSCVNSTELIOQIVAINAGIPLGNT 120  
 DB 61 GATVFALAEQPHIEISQRTTIVIOKOFIISOHSCVNSTELIOQIVAINAGIPLGNT 120  
 QY 61 GATVFALAEQPHIEISQRTTIVIOKOFIISOHSCVNSTELIOQIVAINAGIPLGNT 120  
 DB 61 GATVFALAEQPHIEISQRTTIVIOKOFIISOHSCVNSTELIOQIVAINAGIPLGNT 120  
 QY 121 SNOISHMDGSSFFFGTGTITGFGNISPRTEGKRFCTIVALLGPIPLAGVGO 180  
 DB 121 SNOISHMDGSSFFFGTGTITGFGNISPRTEGKRFCTIVALLGPIPLAGVGO 180  
 QY 121 SNOISHMDGSSFFFGTGTITGFGNISPRTEGKRFCTIVALLGPIPLAGVGO 180  
 DB 121 SNOISHMDGSSFFFGTGTITGFGNISPRTEGKRFCTIVALLGPIPLAGVGO 180  
 QY 181 LGTIFGKGLAKVEDTFIKMNSQTKIRIISTIIIFLFGCVLFVALPAIIFKHIEGMSALD 240  
 DB 181 LGTIFGKGLAKVEDTFIKMNSQTKIRIISTIIIFLFGCVLFVALPAIIFKHIEGMSALD 240  
 QY 241 AITFVYITLTITGFGDYVAGSDIEYLDKPPVWMWIIWGLAVFAVLSMIGDWLRVIS 300  
 DB 241 AITFVYITLTITGFGDYVAGSDIEYLDKPPVWMWIIWGLAVFAVLSMIGDWLRVIS 300  
 QY 241 AITFVYITLTITGFGDYVAGSDIEYLDKPPVWMWIIWGLAVFAVLSMIGDWLRVIS 300  
 DB 241 AITFVYITLTITGFGDYVAGSDIEYLDKPPVWMWIIWGLAVFAVLSMIGDWLRVIS 300  
 QY 301 KKTKEEVEGERAAAEWTAETAEFEKTRRRRLSVEIYDKFORATSIKRLSAELAGNHQ 360  
 DB 301 KKTKEEVEGERAAAEWTAETAEFEKTRRRRLSVEIYDKFORATSIKRLSAELAGNHQ 360  
 QY 301 KKTKEEVEGERAAAEWTAETAEFEKTRRRRLSVEIYDKFORATSIKRLSAELAGNHQ 360  
 DB 301 KKTKEEVEGERAAAEWTAETAEFEKTRRRRLSVEIYDKFORATSIKRLSAELAGNHQ 360  
 QY 361 ELTPCRRITLSVNHLTNERDVLPLPLKTESIYINGLTPHCAGEEIAVENIK 411  
 DB 361 ELTPCRRITLSVNHLTNERDVLPLPLKTESIYINGLTPHCAGEEIAVENIK 411

Db 361 eltpcrrtlsvnhltserdvlppllktesylnltphcageelavlenlk 411

RESULT 3  
ID AAB50044 standard; Protein: 411 AA.  
X X AAB50044:  
X X 19-MAR-2001 (first entry)  
X X Human TREK.  
X X DE Human TREK.  
X X Human; TREK: 2P domain potassium channel; resting membrane potential;  
X X neuronal excitability; neurotransmitter release modulation; epilepsy;  
X X neurological disorder; sleep-related disorder; cognitive dysfunction;  
X X attention deficit disorder; addiction; anxiety; phobia;  
X X Parkinson's chorea; Huntington's chorea; cerebral palsy; incontinence;  
X X erectile dysfunction; alopecia.  
X X Homo sapiens.  
X X OS  
X X WO200072863-A2.  
X X PD 07-DEC-2000.  
X X PF 01-JUN-2000; 2000MO-GH02107.  
X X PR 01-JUN-1999; 99GB-0012733.  
X X PA (SMIK ) SMITHKLINE BEECHAM PLC.  
X X PI Hervieu GJ, Meadows HJ, Randall AD;  
X X WPI: 2001-080422/09.  
X X DR N-PSDB; AAC90412.  
X X PT Use of human TREK1 polypeptide, polynucleotides encoding them and  
X X modulators of h-TREK1 polypeptides for treating epilepsy, sleep-related  
X X disorders, addition and dyskinesias including Parkinson's and  
X X Huntington's chorea  
X X PT Huntington's chorea  
X X PS Claim 7; Page 29; 35pp; English.  
X X CC The present sequence is human TREK1 (h-TREK1). h-TREK1 is a member of the  
X X 2P domain potassium channel family of proteins which play a part in the  
X X control of resting membrane potential. Modulation of these channels will  
X X therefore affect neuronal excitability, thereby leading to a modulation  
X X of neurotransmitter release and activity of neuronal networks. Such  
X X modulation therefore may be useful for the treatment of certain  
X X neurological conditions such as epilepsy, sleep-related disorders,  
X X cognitive dysfunction, attention deficit disorder, addiction,  
X X anxiety/phobia, Parkinson's and Huntington's chorea, cerebral palsy,  
X X incontinence, erectile dysfunction or alopecia.  
X X CC  
X X SQ Sequence 411 AA;

Query Match 99.8%; Score 2095; DB 22; Length 411;  
Best Local Similarity 99.8%; Pred. No. 1.9e-209;  
Matches 410; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAADLLDPKSAONSKPRLSFTRPTVLASRVESDPTINVMKKVTSTFLVVLVLI 60  
Db 1 maadllldpkksaonskprlsftrptvlasrvesdptinvmkkvtstflvvlvli 60

QY 61 GATVFKALEOPHEISORTTIVIOKOTFISOHSCVNSTELDELIOIYVAINAGIIPGNT 120  
Db 61 gatvfkaleqheisqrtlviqkqtfisqhsconsteldelqivaaiaagilipgnt 120

QY 121 SNOISHDLDGSEFFAGVITTTTGFGNISPRTEGGKIFCIITALLGIPLPGFLLAGVGDO 180  
Db 121 snqishwdlgssffagvtlttignisprteggkifciliyaliglipflilagvgd 180

QY 181 LGTIFGKGIANKVEDTFLKMNVSQTKIRIISTIFILFGCVIVVAPLPIFNHIGWSALD 240  
Db 181 lgtifgkiakvedtflkwnvsqtkiristifilfgcvilvalpalfhiegwsald 240

QY 241 AIFVVTITLTITIGRDYVAGSDIEYDFKPPVWFMI; :LAVFAAVLSMIGMLRYS 300  
Db 241 aifvvtitltitigrdyvaagsdleyldfkrpwwfwj; :lavyfaavlsimgmlrvis 300

QY 301 KKTKEEVEGFRAHAEMTANTAEFKETRRRLSVEIYDKFQFATSIKRLSAELAGNHQ 360  
Db 301 kktkeevgefrhaaewantaeefketrtrrlsveiydkfqratsirkksaelagnhq 360

QY 361 ELTPCRRTLVSNHLTNERDVLPPLLKTESIYLNGLTPHCAGEELAVLENIK 411  
Db 361 eltpcrrtlsvnhltserdvlppllktesylnltphcageelavlenlk 411

RESULT 4  
ID AAY28497 standard; Protein: 411 AA.  
X X AAY28497:  
X X AC AAY28497;  
X X DT 12-OCT-1999 (first entry)  
X X DE Mouse h-TREK1 polypeptide.  
X X X X h-TREK1; two pore potassium channel; inflammatory disease;  
X X chromosome 1q32.  
X X OS Mus musculus.  
X X PN WO9937762-A1.  
X X PD 29-JUL-1999.  
X X PF 02-DEC-1998; 98WO-EP07805.  
X X PR 09-OCT-1998; 98GB-0022135.  
X X PR 27-JAN-1998; 98EP-0300570.  
X X PA (SMIK ) SMITHKLINE BEECHAM PLC.  
X X PI Chapman CG, Meadows HJ;  
X X WPI: 1999-469126/39.  
X X DR N-PSDB; AA200040.  
X X PT New two pore potassium channel used for, e.g., treatment of cancer,  
X X pulmonary, cardiovascular and inflammatory diseases  
X X PS Claim 3; Page 26; 44pp; English.  
X X CC This sequence is the mouse h-TREK1 polypeptide encoded by the h-TREK1  
X X polynucleotide AA200040. h-TREK1 is a two pore potassium channel.  
X X CC The polynucleotide sequence of h-TREK1 can be used to diagnose a  
X X disease or susceptibility to a disease related to expression or activity  
X X of h-TREK1 polypeptides. The methods of diagnosis may be used in the  
X X treatment of diseases including cancer, pulmonary, cardiovascular, and  
X X inflammatory diseases, pain, psychiatric disorders including depression  
X X and schizophrenia, neurodegenerative diseases including Alzheimer's,  
X X stroke, and head trauma and neurological disorders including migraine.  
X X CC  
X X SQ Sequence 411 AA;

Query Match 96.9%; Score 2095; DB 20; Length 411;  
Best Local Similarity 95.9%; Pred. No. 3.4e-203;  
Matches 394; Conservative 12; Mismatches 5; Indels 0; Gaps 0;

QY 1 MAADLLDPKSAONSKPRLSFTRPTVLASRVESDPTINVMKKVTSTFLVVLVLI 60  
Db 1 maadllldpkksaonskprlsftrptvlasrvesdptinvmkkvtstflvvlvli 60





PD 10-SEP-1999.  
 XX  
 PF 23-FEB-1999; 99MO-FR00404.  
 XX  
 PR 05-MAR-1998; 98PR-0002725.  
 XX  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 XX  
 PI Honore E, Fink M, Lazdunski M, Lesage F, Duprat F;  
 DR MPI; 1999-551038/46.  
 DR N-PSDB; AA210606.  
 XX  
 PT New mechanically sensitive potassium channel, used to screen for  
 PT specific modulators, potential therapeutic agents for heart and nervous  
 PT system disorders  
 XX  
 PS Claim 2; Fig 1; 40pp; French.  
 XX  
 CC The present sequence represents a mechanically sensitive potassium  
 CC channel protein designated TRAK. The protein is activated by  
 CC polyunsaturated fatty acids, particularly arachidonic acid, and by  
 CC riluzole. The protein is used to screen for specific modulators which  
 CC are useful for treating or preventing diseases of the heart and nervous  
 CC systems in humans and animals, e.g. epilepsy, cardiovascular disease  
 CC (arrhythmia), neurodegeneration (particularly where associated with  
 CC ischemia or anoxia), abnormalities of hormone secretion and muscular  
 CC disease. The protein itself may be used to treat these diseases.  
 CC Antibodies specific for the protein are used to detect it in tissues,  
 CC also as therapeutic inhibitors or activators.  
 CC  
 SO Sequence 398 AA;

Query Match 37.0%; Score 776.5; DB 20; Length 398;  
 Best Local Similarity 49.8%; Pred. No. 3e-72;  
 Matches 142; Conservative 57; Mismatches 83; Indels 3; Gaps 1;

QY 42 MKKNTVSTFLVVLVLIIGATVPEKALEOPHEISQRTTIVIOKOTFISOHCYVNSTELDE 101  
 DB 1 mstctlaialaialylyvsqalvqaleqphqgqakmhdyroqftrdpcvsqskled 60  
 QY 102 LIQOIVAINAIIP--LGNTSNQISHWDLGSSFFPAGTVITTTIGFNGISPRTEGGKIF 158  
 DB 61 flklivealgganpsetwnshssawmlgsaffsgltitlygnlvthdgrlf 120  
 QY 159 CIYALLGIFLFGFLAGVGDQGTIRGKIAYEDTFIKMNSQTKIRIRITIFLFG 218  
 DB 121 ctfayalvgldlfgmlagvdrigssalrrglnhealfkwhvppglvrsisavflilg 180  
 QY 219 CVLPEVALPAILFIKHEGMSALDAIFYVITLTGFGDYVAGSDIYLDPEYKPVWFMI 278  
 DB 181 clifvlptfvtfsweswskleayivltltvgfgydgdygdtgspayqplvfwfwi 240  
 QY 279 LVGFAFAVLISMIGDLRVYISKRTKEVGEFRAHAAEWTANVTA 323  
 DB 241 lfgyayfasvltlignvlavsrtrraemglltaasvgtiva 285

RESULT 9  
 ID AAY28498  
 AC AAY28498; standard; Protein; 107 AA.  
 XX  
 DT 12-OCT-1999 (first entry)  
 DE Partial h-TREK1 polypeptide.  
 KW Partial h-TREK1: two pore potassium channel; inflammatory disease;  
 KW chromosome 1q32.  
 XX  
 OS Homo sapiens.

XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 2 /note= "Encoded by ACC"  
 FT Misc-difference 6 /note= "Encoded by CAA"  
 FT  
 FT  
 FT  
 PN MO9937762-A1.  
 PD 29-JUL-1999.  
 XX  
 PF 02-DEC-1998; 98MO-EP07805.  
 XX  
 PR 09-OCT-1998; 98GB-0022135.  
 PR 27-JAN-1998; 98EP-0300570.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 XX  
 PI Chapman CG, Meadows HJ;  
 DR MPI; 1999-469126/39.  
 DR N-PSDB; AA200041.  
 XX  
 PT New two pore potassium channel used for, e.g. treatment of cancer,  
 PT pulmonary, cardiovascular and inflammatory diseases  
 XX  
 PS Claim 18; Page 25; 44pp; English.  
 XX  
 CC This sequence is a partial h-TREK1 polypeptide encoded by the h-TREK1  
 CC polynucleotide AA200041. AA200039 and AAY28498 are complete h-TREK1  
 CC polynucleotide and polypeptide sequences. h-TREK1 is a two pore  
 CC potassium channel, and the gene maps to human chromosome 1q32, between  
 CC the markers DIS237 and W15105. The polynucleotide sequence of h-TREK1 can  
 CC be used to diagnose a disease or susceptibility to a disease related to  
 CC expression or activity of h-TREK1 polypeptides. The methods of diagnosis  
 CC may be used in the treatment of diseases including cancer, pulmonary,  
 CC cardiovascular, and inflammatory diseases, pain, psychiatric disorders  
 CC including depression and schizophrenia, neurodegenerative diseases  
 CC including Alzheimer's, stroke, and head trauma and neurological  
 CC disorders including migraine.  
 CC  
 SO Sequence 107 AA;

Query Match 26.0%; Score 547; DB 20; Length 107;  
 Best Local Similarity 98.1%; Pred. No. 3.5e-45;  
 Matches 105; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 119 NTSNQISHWDLGSSFFPAGTVITTTIGFNGISPRTEGGKIFCIYALLGIFLFGFLAGVG 178  
 DB 1 usnqyswhwdlgsffagvtltllygfnlsprrteggkifcliyallgplfllagvy 60  
 QY 179 DQIGTFGKIAYEDTFIKMNSQTKIRIRITIFLFGCVLFAVL 225  
 DB 61 dqigtlfgykiayvedtfikmnsqtkiriristliffllgcvlfa 107

RESULT 10  
 ID AAY90356  
 AC AAY90356; standard; Protein; 499 AA.  
 XX  
 DT 04-DEC-2000 (first entry)  
 DE Human TWIK-2 protein.  
 KW Human TWIK-2 protein.  
 KW Human TWIR-3; TWIR-4; TWIR-2; central nervous system disorder; dementia;  
 KW Tandem of P domains in a weak inward rectifying K<sup>+</sup> channel; epilepsy;  
 KW Alzheimer's disease; Parkinson's disease; multiple sclerosis; depression;  
 KW amyotrophic lateral sclerosis; progressive supranuclear palsy; mania;  
 KW Creutzfeldt-Jacob disease; psychiatric disorder; schizophrenic disorder;  
 KW Korsakoff's psychosis; anxiety disorder; phobic disorder; amnesia;

XX	learning disorder; memory disorder; age-related memory loss; obesity;
KW	neurological disorder; cardiac disorder; gene therapy.
XX	
OS	Homo sapiens.
XX	
PN	WC200052164-A2.
XX	
PD	08-SEP-2000.
XX	
PF	01-MAR-2000; 2000MO-US05409.
XX	
PR	01-MAR-1999; 99US-0259951.
XX	
PA	(MILL-) MILLENNIUM PHARM INC.
XX	
PI	Curtis RAJ;
XX	
XX	
DR	WPI; 2000-572183/53.
XX	
DR	N-PDB; AAA37770, AAA37771.
XX	
PT	New tandem of P domains in a weak inward rectifying potassium channel
PT	proteins and genes for e.g. developing therapeutic agents for potassium
PT	channel associated disorders, e.g. central nervous system, psychiatric
PT	disorders -
XX	
PS	Disclosure; Fig 1; 148pp; English.
XX	
XX	This sequence represents the human TWIK-2 protein of the invention. The
CC	channel-2). TWIK-3 and TWIK-4 nucleic acids and proteins are useful as
CC	targets for developing modulating agents to regulate a variety of
CC	cellular processes. They may be useful for developing novel diagnostic
CC	and therapeutic agents for potassium channel associated disorders,
CC	e.g. central nervous system disorders (e.g. Alzheimer's disease,
CC	dementia, Parkinson's disease, multiple sclerosis, amyotrophic lateral
CC	sclerosis, progressive supranuclear palsy, epilepsy, Creutzfeldt-Jacob
CC	disease), psychiatric disorders (e.g. depression, schizophrenia
CC	disorders), Korsakoff's psychosis, mania, anxiety disorders or phobic
CC	disorders), learning or memory disorders (e.g. amnesia or age-related
CC	memory loss), neurological disorders (e.g. migraine, obesity, and
CC	cardiac disorders. The nucleic acids, proteins, protein homologues and
CC	antibodies against them may be further used in screening assays,
CC	predictive medicine. The nucleic acids can be inserted into vectors and
CC	used as gene therapy vectors, to express TWIK protein, to detect TWIK
CC	mRNA, modulate TWIK activity, and screen for drugs or compounds that
CC	modulate TWIK activity. Host cells may be used to produce non-human
CC	transgenic animals.
XX	
XX	
Sequence	499 AA;
50	

[illegible]

Dn	242	vnm-----kvsnf-----vevkhaklkriri-----rkeaf 267
Oy	353	ELAGNHQELTPCRRILSVNHLNERDV--LPPLLTES; 391 + :   :   :   :   : Db 268 e-ssphs-----rkaiqvkxgstaskdvnlfslskker 301
	RESULT 11	
AAV9675	AAV9675 standard; Protein; 499 AA.	
AAV9675;		
29-AUG-2000	(first entry)	
Human potassium channel TASK2.		
TASK2; TWIK-related acid-sensitive K+ chann		
potassium channel; drug screening; hypertensio		
hypotensive; transplant rejection; therapy; diagnosis.		
Homo sapiens.		
Location/Qualifiers		
Key	8..26	
Domain	/note= "transmembrane domain 1"	
FT	113..133	
FT	/note= "transmembrane domain 2"	
FT	158..180	
FT	/note= "transmembrane domain 3"	
FT	229..250	
FT	/note= "transmembrane domain 4"	
FT	85..133	
FT	/note= "P domain"	
FT	190..215	
FT	/note= "P domain"	
Modified-site	77	
/note= "N-glycosylated"		
WC0200027871-A2.		
18-MAY-2000.		
09-NOV-1999;	99MO-IB01986.	
XX PR 09-NOV-1998;	98US-0107692.	
PR 08-NOV-1999;	99US-0436265.	
(CNRS ) CNRS CENT NAT RECH SCI.		
Duprat F, Lesage F, Lazdunski M;		
WPI: 2000-376487/32.		
N-PDB; AAA27747.		
New nucleic acid encoding a non-inactivating outwardly rectifying potassium transport channel, designated TASK2, useful in the treatment of hypertension or dysfunctions of the kidney, liver or pancreas -		
Claim 16; Fig 14a; 91pp; English.		
The present sequence is that of human TASK2 (TWIK-related acid-sensitive potassium channel 2), a novel member of the 2P domain potassium channel family that also includes TWIK-1 (see AAV9673) and TASK1 (see AAV9674). TASK2 is a unique potassium transport channel that is regulated by external pH, and is preponderantly expressed in kidney and epithelial tissues. The invention relates to: identification of the native renal channel; the properties of TASK2; identification of potent pharmacology that specifically modulates the activity of the TASK-2 channel; localizing K+ channels comprising the TASK2 subunit in vivo; and the generation of mice in which the TASK2 gene has been inactivated. The invention also relates to diagnostic tests and therapeutic methods to detect		







PT channel nucleic acids and proteins, useful in assays for identifying  
 PT candidate compounds which are potential pesticides or therapeutics -  
 PS Claim 5; Page 87-88; 96pp; English.

CC The present sequence represents tandem pore domain weak inward potassium  
 CC (K+) polypeptide. The specification describes TWIK2, TWIK3, TWIK4,  
 CC TWIK5, TWIK6, TWIK7, and TWIK1. The TWIK channel nucleic acids and  
 CC proteins are used in screening assays to identify candidate compounds  
 CC which are potential pesticides or therapeutics. The TWIK channel nucleic  
 CC acids can be used for generating mutant phenotypes in animal models or  
 CC in living cells that can be used to study the ion channels, their  
 CC regulation, and their use as pesticide or drug targets, and as  
 CC hybridisation probes and replication/amplification primers. TWIK  
 CC channel proteins are useful as immunogens to generate monoclonal or  
 CC polyclonal antibodies, and in assays to identify molecules that would  
 CC specifically bind to them. Genetically engineered metazoan invertebrate  
 CC animals may be used in studying TWIK channel activity, and for screening  
 CC and identifying new drug targets, therapeutic agents, diagnostics and  
 CC prognosis useful in treating disorders associated with ion channels.

XX Sequence 361 AA:

Query Match 18.2%; Score 382; DB 22; Length 361;  
 Best Local Similarity 35.2%; Pred. No. 3e-31;  
 Matches 88; Conservative 51; Mismatches 89; Indels 22; Gaps 6;

QY 56 LYLIGATVFKALEOPHEISORTTIVIOKOTFISQHSQVNSTELDELIOQIVAINAGIT 115  
 DB 55 mfcsgaavtsyfeapeeralrvklgtavqkflvsnpvndadleeeliveivranngvys 114

QY 116 PLGNTSNQISHWDLGSSFFPAGTIVITTTIGCNISPRTEGSKICITIALGIPFGFLA 175  
 DB 115 alenalse-pnwsfgsfqfaffastvltitgyhvtplsrngklcmfayavqpltlvlls 173  
 QY 176 GVGDQL-GTIFGKGIKAKVEDFPKMNVSQ-----TKRIITSTIIIFLFGCVLVALP 226  
 DB 174 alverllipfv-----llqvlnsklghlyqplrlrlvhlavllvllvfillp 223

QY 227 AILFKHIE-GMSALDAIVFVITLTITGFGDYVAGSDIE-YLDFKPPVWFMIIVGLAY 284  
 DB 224 aaftaslepewdyldstlycfistltlgdyipgsahqpyrplykmtlctylfigilt 283

QY 285 FAAVLSMIGD 294  
 DB 284 mmlltlctfyd 293

RESULT 15  
 AAM23397  
 ID AAM23397 standard; Protein; 336 AA.

XX AAM23397;

XX 17-MAR-1998 (first entry)

XX TWIK-1 potassium channel protein.

XX TWIK-1 potassium channel; screening; diagnosis; transgenic animal;  
 KW Tandem of P domains in a weak inward rectifying K+; antibody.

XX Homo sapiens.

XX FR2744730-A1.

XX 14-AUG-1997.

XX 08-FEB-1996; 96FR-0001565.

XX 08-FEB-1996; 96FR-0001565.

XX (CNRS ) CNRS CENT NAT RECH SCI.

XX Barbanin J, Duprat F, Fink M, Guillemare J, Lazdunski M;  
 PI Lesage F, Romey G;  
 XX  
 XX  
 DR MPI: 1997-427773/40.  
 N-PSDB; AAT64960.

PT Nucleic acid encoding new potassium channel designated TWIK-1 -  
 PT useful for treating channel deficiency diseases, screening for  
 PT active agents and for diagnosis

XX Claim 12; Figure 1b; 37pp; French.

XX The present sequence represents a protein consisting a potassium channel  
 CC with the properties of a TWIK (Tandem of P domains in a weak inward  
 CC rectifying K+-1 channel. This is the first member of a new family of  
 CC channels consisting of 4 transmembrane segments and two P domains, and  
 CC being only weakly rectifying. The CDNA, vectors, the cells expressing  
 CC TWIK-1 type channels and the protein are used to compensate  
 CC for deficiency of potassium channels in various tissues. Compounds  
 CC for modulating activity of TWIK-1 type channels may also be useful  
 CC therapeutically, e.g. for control of epilepsy, arrhythmia, vascular  
 CC disease, neurodegeneration (particularly of ischaemic or anoxic origin),  
 CC endocrine or muscular disorders. The CDNA and the vectors can also be  
 CC used to create transgenic animals (especially knock-out animals) for use  
 CC as models of TWIK-1 related diseases. Analysis of the sequence of the  
 CC TWIK-1 gene may be used for pre-natal diagnosis of disease. Antibodies  
 CC can be used to detect TWIK-1 channels and for inhibiting or activating  
 CC the channels in vivo.

XX Sequence 336 AA:

Query Match 18.1%; Score 379.5; DB 22; Length 336;  
 Best Local Similarity 32.5%; Pred. No. 4.9e-31;  
 Matches 90; Conservative 62; Mismatches 28; Indels 17; Gaps 9;

QY 51 FLVV-VLYLIGATVFKALEOPHEISORTTIVIOKOTFISQVNSTELDELIOQIVA 108  
 DB 25 flvlyllylvfsgavfssvelpyedllrgelrkrlrlly heclseqqlqfgrve 84

QY 109 AINAGIIPGNTSNQISHWDLGSSFFPAGTIVITTTIGCNISPRTEGSKICITIALGIP 168  
 DB 85 asnygvslnasgn-wndftsalffastvltitgyhvtplsrngklcmfayavqpltlvlls 143

QY 169 LRFELLAGYGDQGTIFGKGIKAKVEDFPKMNVSQRIKIRISII--FILFGCVLVALP 226  
 DB 144 fclllflavavgrltvhtcr--rpvlyfhlrtwgfsgkqvavilvhlvgtvcscffli-p 199

QY 227 AILFKHIE-GMSALDAIVFVITLTITGFGDYVAG-GSDIEVLDFFKPPVWFMIIVGLAY 284  
 DB 200 aavfsvldeedwntlesfyctfistltlgdyipgsahqpyrplykmtlctylfigilt 259

QY 285 FAAVLSMIGDMLRVISK-----KTKEVEGEFRHAAE 315  
 DB 260 mlvletfce-lhelkkfrkmfyvkkkdedqyhlle 255

Search completed: August 28, 2001, 17:05:46  
 Job time: 1891 sec



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A:Map position: 5  
A:introns: 28/3; 76/3; 184/2; 217/2; 270/2; 295/2

Query Match 13.7%; Score 288; DB 2; Length 383;

Best Local Similarity 23.6%; Pred. No. 1e-15;

Matches 85; Conservative 80; Mismatches 127; Indels 68; Gaps 12;

```

OY 20 LSEFTKPTVLASRVESDPTITNMKMKT-VSTIFLVVLYLIGATVFKALQEPHEISQRT 78
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 16 LRANTLPSTIRARVGCARLRIRYEENARFYLICILILYLAFAILFPHLMEHEVEDERT 75

OY 79 TI---VIQKFTISQHSVCNSTELDELIOQIVAINAGIIPLGNTSNOISHWDLGSSPFF 135
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 76 AIDNRMDYQKVCYCKHKPLNECDPEEMVRFISQATSGLL-----NSRRPDLHLSLF 129

OY 136 AGVITTTIGGNISPRREGKICITIALG----IPLEFFLAGVDDOCTIFGKCIATK 191
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 130 SATVISTIGTGTPTPHLRFTIYGVGCTCCVLFNMLF---ERLVGTGMSYLLRS 185

OY 192 VEDTFIKMNSQTKIRIISTII-----FILFG-CVLFV 223
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 186 LRERKIRYRLAKESGNKPVITLLNEDPNESSCGGMDMWRSPYKVFILFSMCLVLI 245

OY 224 ALPAIIFKHIEGNSALDAIYFVITLTIGFGDYVAGSDIEYL--DFYKPYVWFMLVG 281
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 246 TASAGIYSVENNNYIDSLYCFISFATIGFGDYVNOQDVTRMSPDLYKFFVNCCLTLG 305

OY 282 LAIF-----AAVLSMIGWMLRVISKTKKEVEGEFRHAHAEMTANVTAEFKERRLSV 334
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 306 ACFFYCLSNVSSIVVROLNMM--IKKMDVKV-EDRSFLC-----FKKRRRYMGL 352

```

# RESULT 6

TI9860

hypothetical protein C40C9.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000

C:Accession: T19860

R:Hemby, C.

submitted to the EMBL Data Library, March 1996

A:Reference number: Z19188

A:Accession: T19860

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-334 <WIL>

A:Cross-references: EMBL:270266; PIDN:CAA94204.1; GSPDB:GN00028; CESP:C40C9.1

A:Experimental source: clone C40C9

C:Genetics:

A:Gene: CESP:C40C9.1

A:Map position: X

A:introns: 34/1; 60/2; 98/1; 145/3; 160/3; 181/1; 204/1; 252/2; 279/2; 306/3

Query Match 13.5%; Score 284.5; DB 2; Length 334;

Best Local Similarity 27.4%; Pred. No. 1.7e-15;

Matches 86; Conservative 63; Mismatches 112; Indels 53; Gaps 11;

```

OY 50 IFLVVLYLIGATVFKALQEPHEISQRTIV---IQKQFISQHSVCNSTELDELIOQI 106
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 14 LILSTFYLLFGAMVFPKLE-----SEKQVWVDEIERIDRLKHK-YNSEERDLHFEA 67

OY 107 VAINAGIIPLGNTSNOISHWDLGSSFPAGVITTTIGGNISPRREGKICITIAL 165
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 68 IA-----IKSIPOAGYOMQFAGAFYATVITTVGGHSAFSTNACKLFCMIFALF 119

OY 166 GIPLEFFLAGVDDOCTIFGKCIATKEDTFIK-----MNSQTKRIIS-TIIFLFG 218
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 120 GVPMLGIMFOSIGBRVTFAYLSLHKFRDSLHQOGFTCLQEVPTPHLWVSLTIGFVW-- 177

OY 219 CVLFPALPITFKHIEGNSALDAIYFVITLTIGFGDY--AGSDIEYLDYKPYVWF 276
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 178 ----IVSGTYMFTIEKMSIFDAYYFCMIFSTIGFDLPLQOVNALQDQPLYVFATIM 233

```

```

OY 277 WILVGLAYFAVLISMIGDWLRVLSKTKKEVEGEFRHAHAEMTANVTAEFKERRLSVEI 336
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 234 FILIGLAVFACVNL-----VLGFMASSADLVIA-----AQREPPSAIV 273

```

```

OY 337 YDKFORATSIKRL 350
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 274 LERFTNSLVDSOI 287

```

# RESULT 7

T43361

probable potassium channel chain n2p20 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 11-Jan-2000

C:Accession: T43361

R:Mang, Z.W.; Salkoff, L.

submitted to the EMBL Data Library, August 1998

A:Description: Potassium channels in C. elegans.

A:Reference number: Z22450

A:Accession: T43361

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-364 <MAN>

A:Cross-references: EMBL:AF083646; PIDN:AC32857.1

Query Match 13.5%; Score 284.5; DB 2; Length 364;

Best Local Similarity 27.4%; Pred. No. 1.9e-15;

Matches 86; Conservative 63; Mismatches 112; Indels 53; Gaps 11;

```

OY 50 IFLVVLYLIGATVFKALQEPHEISQRTIV---IQKQFISQHSVCNSTELDELIOQI 106
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 14 LILSTFYLLFGAMVFPKLE-----SEKQVWVDEIERI-LKHK-YNSEERDLHFEA 67

OY 107 VAINAGIIPLGNTSNOISHWDLGSSFPAGVITTTIG-MSIPREGKICITIAL 165
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 68 IA-----IKSIPOAGYOMQFAGAFYATVITTVGGHSAFSTNACKLFCMIFALF 119

OY 166 GIPLEFFLAGVDDOCTIFGKCIATKEDTFIK-----MNSQTKRIIS-TIIFLFG 218
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 120 GVPMLGIMFOSIGBRVTFAYLSLHKFRDSLHQOGFTCLQEVPTPHLWVSLTIGFVW-- 177

OY 219 CVLFPALPITFKHIEGNSALDAIYFVITLTIGFGDY--AGSDIEYLDYKPYVWF 276
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 178 ----IVSGTYMFTIEKMSIFDAYYFCMIFSTIGFDLPLQOVNALQDQPLYVFATIM 233

OY 277 WILVGLAYFAVLISMIGDWLRVLSKTKKEVEGEFRHAHAEMTANVTAEFKERRLSVEI 336
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 234 FILIGLAVFACVNL-----VLGFMASSADLVIA-----AQREPPSAIV 273

OY 337 YDKFORATSIKRL 350
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 274 LERFTNSLVDSOI 287

```

# RESULT 8

T43394

potassium channel chain n2p18 homolog - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 21-Jan-2000

C:Accession: T43394

R:Kunkel, M.T.; Salkoff, L.

submitted to the EMBL Data Library, August 1998

A:Description: Potassium channels in C. elegans.

A:Reference number: Z22479

A:Accession: T43394

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-461 <KUN>

A:Cross-references: EMBL:AF083650; PIDN:AC32861.1





A:Description The sequence of C. elegans cosmid C24A3.  
A:Reference number: Z18373  
A:Accession: T15594  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-325 <FAA>  
A:Cross-references: EMBL:U040424; NID:g1065542; PID:g1065543; PIDD:AA81455.1; CESP:C24A3  
C:Genetics:  
A:Gene: CESP:C24A3.6  
A:introns: 21/1; 63/3; 131/1; 193/3; 206/3

Query Match            12.8%; Score 269; DB 2; Length 325;  
Best Local Similarity   25.1%; Pred. No. 2.9e-14;  
Matches   86; Conservative   53; Mismatches   88; Indels   116; Gaps   11;

OY   46 TVSTIF-----LVVLYLIIGATVKALDEPHISORTIVIOKQFISOHSCVN   95  
     | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
Db   10 TLTFQKTPFKGLPLPIILVAFTLLGAVIPMMIBENE-----REMLIEOK---   56  
OY   96 STEDELIIQOIYAIAIN-----AGIIPLGNTNOIS   125  
     | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
Db   57 --ERELRLRRYYKKINOLQRKRRLMTAEERYNRTANVLTTFOETLGIIVA--DMDDDI   112  
OY   126 HHMDGSSEFFAGVTITTGFGNISPRTEGKIPICIYALLGIPLEGFLACVGDLGTIF   185  
     | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
Db   113 HMTFGSIFYCKTIVITTYGGINVPCTGMGRPATILVAFIGIPVLVSly----CLGSLF   168  
OY   186 GKGIKAKVEDTFIKMNVSOtkIRIIS-----   210  
     | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
Db   169 AKGCKMLRFLK-----STRVYSKDLNNKISEADNIIEGTTAITPSAEKTENNDDL   222  
OY   211 ---TIIFLCGCVFVALPAIFKHIEGMSALDAIYFVVITLTTFGFDGYVAGSDIEYL   267  
     | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
Db   223 LSPFISSLTLITVIWICAVLFLEFEWDEFTSLYFTLISFTTIGFDIIP--SDYDFM   280  
OY   268 DEYKPVWFMIYGLAYFAAVLSMGDWLRVIS-----KKRKE   305  
     | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
Db   281 ----PIGVLLILGISLVSTVWTLLIQOOIEALASVRRKKKKK   319

RESULT   12  
T24265  
hyocheical protein T01B4.1 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence revision 15-Oct-1999 #text change 18-Feb-2000  
C:Accession: T24265  
R:Wilkinson, J.  
submitted to the EMBL Data Library, March 1996  
A:Reference number: Z19866  
A:Accession: T24265  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-522 <WILL>  
A:Cross-references: EMBL:Z70036; PIDD:CAA93875.1; GSPDB:GN00028; CESP:T01B4.1  
A:Experimental source: clone T01B4  
C:Genetics:  
A:Gene: CESP:T01B4.1  
A:Map position: X  
A:introns: 95/3; 142/1; 224/3; 290/1; 458/1

Query Match            12.7%; Score 266; DB 2; Length 522;  
Best Local Similarity   23.1%; Pred. No. 9e-14;  
Matches   99; Conservative   64; Mismatches   132; Indels   134; Gaps   15;

OY   50 IFLVVLYLIIGATVKALEOPHE-----ISRTTIVIOKQFISOHSCVNSTE   98  
     | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
Db   41 LILILGACLGCVGFQALDYDOOLELAERKRVLSSESLAVNLLEHLQMNGOSNE   100  
OY   99 IDELIQOIVAAINAGIIPLGNTS--MOISHMDGSSEFFAGVITTYIGGNSIPREGGIK   157  
     | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
Db   101 -----KRCIELTKTFIORSDERGEGRWDPMNVFSATILETTITGIGNACKTNIGRI   155

[illegible]





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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compen Ltd.

OM protein - protein search, using sw model

Run on: August 28, 2001, 17:05:51 ; Search time 54.36 Seconds  
(without alignments)  
1000.319 Million cell updates/sec

Title: US-09-503-089a-2  
Perfect score: 2100  
Sequence: 1 MAAPDLDPKSAONSKPRL.....LNGILPMGAGEIAVENIK 411

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues  
Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: SPREMBL\_16:\*  
2: sp\_archaea:\*  
3: sp\_bacteria:\*  
4: sp\_fungi:\*  
5: sp\_human:\*  
6: sp\_invertebrate:\*  
7: sp\_mammal:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_unclassified:\*  
13: sp\_vertebrate:\*  
14: sp\_virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2095	99.8	411	4	Q9NRT2
2	1249	59.5	538	11	Q9JIS4
3	1243	59.2	538	4	Q9HBS9
4	502.5	23.9	284	4	Q9H591
5	412.5	19.6	502	11	Q9UK62
6	378.5	18.0	336	11	Q9JL58
7	357.5	17.0	365	11	Q9JL58
8	356.5	17.0	259	6	Q02821
9	349.5	16.6	374	4	Q9NRC2
10	347.5	16.5	330	4	Q9HBC8
11	345	16.4	329	5	Q76795
12	343	16.3	313	11	Q9ERU5
13	342.5	16.3	229	4	Q9H592
14	341	16.2	395	11	Q9JL58
15	339.5	16.2	330	4	Q9H427
16	336	16.0	289	11	Q9GX34
17	331.5	15.8	336	5	Q17185
18	328.5	15.6	237	11	Q9ES08
19	304.5	14.5	430	4	Q9HBI5

20	301	14.3	430	11	Q9ERS1
21	300	14.3	340	5	Q9VHE0
22	299.5	14.3	343	11	Q9JL14
23	296.5	14.1	398	5	Q9VPS9
24	293.5	14.0	392	11	Q9ESM5
25	288	13.7	383	5	Q21094
26	287.5	13.7	408	4	Q9HBI4
27	284.5	13.5	364	5	Q9VY75
28	284.5	13.5	385	5	Q9VY75
29	282.5	13.5	461	5	Q9VY75
30	280	13.3	405	11	Q9ERS0
31	279	13.3	393	5	Q9XU07
32	273	13.0	392	5	Q9NEV3
33	273	13.0	1910	5	Q22426
34	269	12.8	325	5	Q18120
35	266	12.7	522	5	Q22042
36	262	12.5	452	5	Q93531
37	261.5	12.5	395	5	Q9V362
38	249.5	11.9	427	5	Q23386
39	247	11.8	444	5	Q45891
40	245.5	11.7	1539	5	Q19611
41	244.5	11.6	513	5	Q22940
42	243.5	11.6	270	11	Q9JL57
43	243	11.6	389	5	Q9VE68
44	240	11.4	524	5	Q21729
45	236.5	11.3	654	5	P90863

## ALIGNMENTS

RESULT	1	PRELIMINARY:	PRT:	411 AA.
Q9NRT2	09NRT2			
AC	Q9NRT2;			
DT	01-OCT-2000 (Tremblrel. 15, Created)			
DT	01-OCT-2000 (Tremblrel. 15, Last sequence update)			
DT	01-MAR-2001 (Tremblrel. 16, Last annotation update)			
DE	TWO-PORE DOMAIN POTASSIUM CHANNEL TREK-1.			
GN	TREK-1.			
OS	Homo sapiens (human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=BRAIN;			
RA	Meadows H.J., Benham C.D., Cairns W., Gloger J., Jennings C.,			
RA	Medhurst A.D., Murdoch P., Chapman C.G.;			
RT	"Cloning, localization and functional expression of the human ortholog			
RT	of the TREK-1 potassium channel."			
RL	Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: AF171068; AAF89743.1; -;			
DR	InterPro: IPR001622; -;			
DR	InterPro: IPR003280; -;			
DR	PRINTS: PR01333; ZPROKCHANEL.			
KW	Ionic channel.			
SQ	SEQUENCE 411 AA; 45494 MW; FDE40CAB21B4<AT> CRC64;			

Query Match	99.8%; Score 2095; DB 1	Length 411;
Best local Similarity	99.8%; Pred. No. 7.1e-143;	
Matches 410;	Conservative 1;	Mismatches 0; Indels 0; Gaps 0;
QY	1	MAAPDLDPKSAONSKPRLSFTKPTVLASRVESDPT NVKKRTVSTFLVVLII 60
DB	1	MAAPDLDPKSAONSKPRLSFTKPTVLASRVESDPT NVKKRTVSTFLVVLII 60
QY	61	GATYFKALQPHETISQRTTIVIQKPTISQHSQVNSTELHEI IQQIYAANAGIPLGNT 120
DB	61	GATYFKALQPHETISQRTTIVIQKPTISQHSQVNSTELHEI IQQIYAANAGIPLGNT 120
QY	121	SNQISHWDLGSSFEFACTVITITIGFGNISPRTEGKIFV LGLIPFCFLLAGVDQ 180

RESULT	2		
09JIS4			
ID	09JIS4	PRELIMINARY;	PRT; 538 AA.
AC	09JIS4;		
DT	01-OCT-2000 (TREMblrel. 15, Created)		
DT	01-OCT-2000 (TREMblrel. 15, Last sequence update)		
DT	01-MAR-2001 (TREMblrel. 16, Last annotation update)		
DE	POSSASSIUM CHANNEL TREK-2.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_TaxID=10116;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=20298807; PubMed=10747911;		
RA	Bang H., Kim Y., Kim D.,		
RT	"TREK-2, a new member of the mechanosensitive tandem-pore K+ channel		
RT	family,"		
RL	J. Biol. Chem. 275:17412-17419(2000).		
DR	EMBL; AF196965; AAF5132.1; -		
DR	InterPro: IPR000009; -		
DR	InterPro: IPR001622; -		
DR	InterPro: IPR003280; -		
DR	Pfam; PF02034; TWIK_channel; 1.		
DR	PRINTS; PR01333; ZP0RECHANEL.		
QO	SEQUENCE 538 AA; 59800 MW; 1FF33FOAAS2B97E4 CRC64;		

	Query Match	59.5%	Score 1249	DB 11	Length 538
	Best Local Similarity	63.7%	Pred. No. 6.2e-82		
	Matches 247	Conservative 55	Mismatches 64	Indels 22	Gaps
QY	2 AARDLPDKSA--QONSKPRLSFSTKRPVLASRVESDT--TIVMKMKIVSTFICLVVL	56			
Db	23 AARVQCRKSTNHNHPRVLRISIRATFYVA-RHEGSGOGLOTVAKMKIVVALFVVVVV	81			
QY	57 YLIIGATVFKALEORPHEISORTTIVIOKTFIISOHSGVNSTEDELIOQIVAAINMGIIP	116			
Db	82 YLVGGLVFRALREQPFSSQKNTALEKAEPLRHICVSPQELETLQNALDADNMGVSP	141			
QY	117 LGNTSNQISHHDLQSSFFPAGTIVTTTIGFNISPRTEGKIFCTIYALALCIPLEGLLAG	176			
Db	142 VGNSSNSSHHDLQSAFFPAGTIVTTTIGVGNIASTEGGKIFCTIYAFIPLFGFLLAG	201			
QY	177 VGDDLGITFGGINKVBDTFLKMNVSOTFKIRITSTIIFELGCVLPALPAILFEKHTEGM	236			
Db	202 IGDGLGITFGKSIARVKKVSVOTFKIRIVSTIIFELAGCIVFTPIAVLFEKIEGM	261			
QY	237 SALDAIFVVVLTLTITIFCGYVAG--SDIEYLDYKRVVFMVILVGLATYPAALVSMIGM	295			
Db	262 TALSITFVVVLTLTTFVGDFGVAGGNAGINRYEMTKRLVFMVILVGLATYPAALVSMIGM	321			
QY	296 LRVISKTKTEEVGEFRAHAEMWTANVTAEKETRRLSVEIYDKFORAVSIKRLSAAELA	355			

RESULT	3			
09HB59	ID	09HB59	PRELIMINARY;	PRT; 538 AA.
AC	09HB59			
DT	01-Mar-2001	(Tremblrel, 16, Created)		
DT	01-Mar-2001	(Tremblrel, 16, Last sequence of the)		
DT	01-Mar-2001	(Tremblrel, 16, Last annotation)		
DE	2P DOMAIN POTASSIUM CHANNEL TREK2.			
GN	KCNK10.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
FX	MEDLINE=20435789; PubMed=10880510;			
RA	Lesage F., Terrienolre C., Romey G., Lazdunski S.,			
RT	"Human TREK2, a 2P domain mechano-sensitive channel with multiple			
RT	regulations by polyunsaturated fatty acids, phospholipids and Gs,			
RT	G1, and Gq protein-coupled receptors.";			
RL	J. Biol. Chem. 275:28398-28405(2000).			
DR	EMBL; AF279890; AAC15191.1; --			
DR	IONIC channel.			
QO	SEQUENCE 538 AA; 59764 MW; 8BA615B0BD147; CRC64;			

[illegible]









Matches 93; Conservative 56; Mismatches 93; Indels 34; Gaps 11;

OY 42 MKKRTSTFLVY--VLYLIIGATVEKALQPHISORTTIVIOKQFISCHSVNSTEL 99  
 DB 1 MKKNTRTISLITCTLYLVGAAPDALETENILQKLVORREKLKRYMNSNA-DY 59  
 OY 100 DELIIOQVAIA--NAGIIPLGNTSNOISHWDLGSSFFACTVITTTIGFNGISPRTEGKI 157  
 DB 60 EILEATIVKSVPHKAGY-----QMKFSGAFYFATVTITTTIGFNGISPRTEGKI 108  
 OY 158 FCIITVALLGIPLEGFLLAGVGDQGITFGKIAKVEDTFIKMNVSGTKIRIITIFILF 217  
 DB 109 FCMILYALAGIPLEGFLLAGVGDQGITFGKIAKVEDTFIKMNVSGTKIRIITIFILF 163  
 OY 218 GC-VLFPALPAIFIKHIEGMSALDAIFVVTITTTIGFNGYVA---GGS---DIEVLDY 270  
 DB 164 GNGGLIFGAGFMSSTENNTYFDAYTCVTLTTIGFGDYVALQKRGSLQTOPEYV-FE 222  
 OY 271 KPVWFWIIVGLAVFAVLSMIGDMLRVISKKTREE 306  
 DB 223 SLV---FILFGLVISAAMNL--VLRFILMNTDE 253

## RESULT 12

OY 09ERUS PRELIMINARY; PRT; 313 AA.  
 AC 09ERUS;  
 DT 01-MAR-2001 (Tremblrel. 16, Created)  
 DT 01-MAR-2001 (Tremblrel. 16, last sequence update)  
 DE 2P DOMAIN K+ CHANNEL TWIK-2.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 NC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NCBI\_TaxID=10116;  
 RN 11  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SPRAGUE-DAWLEY;  
 RX MEDLINE=20435832; PubMed=10887187;  
 RA Patel A.J., Mangret F., Magnone V., Fosset M., Lazdunski M.,  
 RA Honore E.;  
 RT "TWIK-2, an inactivating 2P domain K+ channel."  
 RL J. Biol. Chem. 275:28722-28730(2000).  
 DR EMBL: AF281304; AAG10508.1; -  
 KW Ionic channel.  
 SQ SEQUENCE 313 AA; 34214 MW; A93629568785CD8F CRC64;

Query Match 16.3%; Score 343; DB 11; Length 313;  
 Best Local Similarity 32.2%; Pred. No. 4e-17;

Matches 77; Conservative 47; Mismatches 107; Indels 8; Gaps 4;

OY 57 YLIIGATVEKALQPHISORTTIVIOKQFISCHSVNSTELDELIOQVAIIMGITP 116  
 DB 17 YLIIGALVRLERPHARLAEIGTLREQLRHSPCAVAHALDAFYERVLGRLGRAV 76  
 OY 117 LGNTSNOIS---HWDLGSSFFAGVITTTIGFNGISPREGKICFIIVALLGIPFGF 172  
 DB 77 LANASCPANSDPAMDAASLFFASLVTWGGYTPRLTDAGKASIVALLGVPITML 136  
 OY 173 LLAGVGDQGITFGKIAKVEDTFIKMNVSGTKIRIITIFILFGLVFPALPAIFKH 232  
 DB 137 LITVAAQRLSLTLH--APLSWLSLRKGMHROAARHVALMIVAIIFLIPAAVFAV 194  
 OY 233 I-EGMSALDAIFVVTITTTIGFGDYVAGSDIE-YIDFKPVVWITVILGLAFVAVL 289  
 DB 195 LBEAMSLDAIFCFISLSTIGLDYVGEAPQPYRSLKVLVTAVLFLGLVAMVVL 253

## RESULT 13

OY 09H592 PRELIMINARY; PRT; 229 AA.  
 AC 09H592;

DT 01-MAR-2001 (Tremblrel. 16, Created)  
 DT 01-MAR-2001 (Tremblrel. 16, last sequence update)  
 DT 01-MAR-2001 (Tremblrel. 16, last annotation update)  
 DE DJ137FL.1 (NOVEL MEMBER OF THE POTASSIUM CHANNEL SUBFAMILY K )  
 DE (FRAGMENT).  
 GN DJ137FL.1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 NC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NCBI\_TaxID=9606;  
 RN 11  
 RP SEQUENCE FROM N.A.  
 RA Williams S.;  
 RL Submitted (SEP-2000) to the EMBL/Genbank/DDBJ databases.  
 DR EMBL: AL136087; CAC07335.1; -  
 KW Ionic channel.  
 FT NON\_TER 229  
 FT SEQUENCE 229 AA; 25344 MW; 7AB9FB847F2422E CRC64;

Query Match 16.3%; Score 342.5; DB 11; Length 229;  
 Best Local Similarity 36.4%; Pred. No. 3e-17;

Matches 79; Conservative 44; Mismatches 11; Indels 15; Gaps 6;

OY 48 STFLVY--VLYLIIGATVEKALQPHISORTTIVIOKQFISCHSVNSTELDELIOQ 105  
 DB 21 STVLLALAYLATIGVFTLEGRAADSSRFGRDK--ONTCLDRALDRLND 80  
 OY 106 IVAIINAGIIPLGNTSNOISHWDLGSSFFACTVITTTIGFNGISPRTEGKICFIIVALL 165  
 DB 81 VVQAYKNGASLISNTTS-MGRMELVGSFFSVSTITIGFNGISPRTEGKICFIIVALL 139  
 OY 166 GIPLEGFLLAGVGDQGITFGKIAKVEDTFIKMNVSGTKIRIITIFILFGLV 221  
 DB 140 GIPNLVVL---NRLGHLMQGVNHWASRLGTF--WD--DPDKARMLAGSGALLSGLL 191  
 OY 222 FVALPAIFKHIEGMSALDAIFVVTITTTIGFGDYV 254  
 DB 192 FLLPPLFLSHMGMSYTEGFYAFITLSTVGRGDYV 222

## RESULT 14

OY 09JUD4 PRELIMINARY; PRT; 395 AA.  
 AC 09JUD4;  
 DT 01-OCT-2000 (Tremblrel. 15, Created)  
 DT 01-OCT-2000 (Tremblrel. 15, last sequence update)  
 DE 01-MAR-2001 (Tremblrel. 16, last annotation update)  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 NC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NCBI\_TaxID=10116;  
 RN 11  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=CEREBELLUM;  
 RX MEDLINE=20200422; PubMed=10734076;  
 RA Kim Y., Bang H., Kim D.;  
 RT "TASK-3, a New Member of the Tandem Pore K+ Channel Family."  
 RL J. Biol. Chem. 275:9340-9347(2000).  
 DR EMBL: AF192366; AAF60229.1; -  
 DR InterPro: IPR000099; -  
 DR InterPro: IPR001622; -  
 DR InterPro: IPR003092; -  
 DR InterPro: IPR003280; -  
 DR Pfam: PF02034; TWIK\_channel.1.  
 DR PRINTS: PRO1333; 2PORECHANNEL.  
 DR PRINTS: PRO1095; TASKCHANNEL.  
 SQ SEQUENCE 395 AA; 44365 MW; 3F76F7923A3AFC7; CRC64;

Query Match 16.2%; Score 341; DB 11; Length 395;  
 Best Local Similarity 30.3%; Pred. No. 7.5e-17;

Matches 93; Conservative 59; Mismatches 111; Indels 44; Gaps 10;

Search completed: August 28, 2001, 17:12:45  
Job time: 414 sec

```
QY 42 MKKRTVSTFLV--VLLYLIGATVFALEQPHIEISORTTIVIOKQFIQSHSCVNSTEL 99
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 1 MKRQNVRLSLIACTFTYLLVGAVALFADLESDHMREREKAKAEVRLRGKYN-ISSDY 59
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 100 DELIQOIVAA--INAGIIPIGNTSNQISHWDGSSFFPAGTIVTTIGFNGISPRTEGGKI 157
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 60 QOLEVLIOSEPHRAGV-----QMFAGSFFFAITVITTTIGYGHAAAGCTDAGKA 108
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 158 FCIIYALIGTLPFGFLAGVGDOLGTIFGKIAVEDTIFKW-----NVSOTKIRI 208
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 109 FCMFYAVAGIPLTLVWFQSLGERM-----NTEFVRLKRIKCCGMRNTEVSM 156
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 209 ISTIIFLFCGCVLFVALPAIFKHIEGMSALDAIFVYITLTITIGFGDYVAGSD--IEY 266
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 157 ENMTYVGFSCMGIVPW-AAAFSCEDMSFFPHAYTCFTITTTIGFDVALQSKGALOR 215
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 267 LDEFKPVWEMILVGLVFAVLSMIGDMLRVISKTKREEV--GEFRAHAEWTANTYAE 324
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 216 KPFYVAFSFMILVGLVIGAFNLV--VLRFLTMNTEDELEGEVAQIILAGNPRRVVR 273
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 325 FKETRRR 331
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 274 VPQSRKR 280
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
```

## RESULT 15

```
Q9H427
ID Q9H427 PRELIMINARY; PRT; 330 AA.
AC Q9H427;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE D1781B1.1 (A NOVEL PROTEIN SIMILAR TO THE ACID-SENSITIVE POTASSIUM
   CHANNEL PROTEIN TASK (KCNK3)).
GN D1781B1.1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lovell J.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL118522; CAC14068.1; -; 24F428721A1C7790 CRC64;
SQ SEQUENCE 330 AA; 36222 MW; 24F428721A1C7790 CRC64;
```

Query Match 16.2%; Score 339.5; DB 4; Length 330;  
Best Local Similarity 34.5%; Pred. No. 7,7e-17;  
Matches 90; Conservative 42; Mismatches 96; Indels 33; Gaps 9;

```
QY 50 IFLVVLYLIGATVFALEQPHIEISORTTIVIOKQFIQSHSCVNSTELDELIQOI 106
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 11 LVLTCLCYLVGAVALFADLESEAE--SGRQLLVOKRGALRRKFGESADYRELRLALQ- 68
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 107 VAATNAGIIPIGNTSNQISHWDGSSFFPAGTIVTTIGFNGISPRTEGGKIFCIITVALG 166
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 69 AEPHRAAG-----RQMKFPGSFFFAITVITTTIEYGHAAAGCTDQSKVCFMAYALG 117
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 167 IPLFGFLAGVGDOLGTIFGKIAVEDTF--IKWNSQTKIRITSTIIFLFCGCVLFVAL 225
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 118 IPLVLTVFQSGISGERLNVNRRLLAAKCCGLRMTCVSTE---NLVYAGLLACATIAL 173
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 226 PAIFKHIEGMSALDAIFVYITLTITIGFGDYVAGSDIEYLDYKPYWVF--WILVGL 282
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 174 GAVAFSHFEGEFPFHAYVYCFITTTIGFGDVALQSG--EALQKRKLPHYVAFSFLYILLGL 232
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 283 AYFAAVLSMT-----GDM 295
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 233 TVIGAFNLVLYLFLVASADW 253
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
```



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 28, 2001, 17:05:46 ; Search time 47.95 Seconds

(without alignments)  
519,634 Million cell updates/sec

Title: US-09-503-089a-4

Perfect score: 2090  
Sequence: 1 MAAPDLDPKSAQNSKPRLL.....LNGLPHCAGEDIAVENKK 411

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

1: A.Geneseq\_0601: \*  
2: /SIDSB/gcgdata/geneseq/geneseq/AA1980.DAT: \*  
3: /SIDSB/gcgdata/geneseq/geneseq/AA1981.DAT: \*  
4: /SIDSB/gcgdata/geneseq/geneseq/AA1982.DAT: \*  
5: /SIDSB/gcgdata/geneseq/geneseq/AA1983.DAT: \*  
6: /SIDSB/gcgdata/geneseq/geneseq/AA1984.DAT: \*  
7: /SIDSB/gcgdata/geneseq/geneseq/AA1985.DAT: \*  
8: /SIDSB/gcgdata/geneseq/geneseq/AA1986.DAT: \*  
9: /SIDSB/gcgdata/geneseq/geneseq/AA1987.DAT: \*  
10: /SIDSB/gcgdata/geneseq/geneseq/AA1988.DAT: \*  
11: /SIDSB/gcgdata/geneseq/geneseq/AA1989.DAT: \*  
12: /SIDSB/gcgdata/geneseq/geneseq/AA1990.DAT: \*  
13: /SIDSB/gcgdata/geneseq/geneseq/AA1991.DAT: \*  
14: /SIDSB/gcgdata/geneseq/geneseq/AA1992.DAT: \*  
15: /SIDSB/gcgdata/geneseq/geneseq/AA1993.DAT: \*  
16: /SIDSB/gcgdata/geneseq/geneseq/AA1994.DAT: \*  
17: /SIDSB/gcgdata/geneseq/geneseq/AA1995.DAT: \*  
18: /SIDSB/gcgdata/geneseq/geneseq/AA1996.DAT: \*  
19: /SIDSB/gcgdata/geneseq/geneseq/AA1997.DAT: \*  
20: /SIDSB/gcgdata/geneseq/geneseq/AA1998.DAT: \*  
21: /SIDSB/gcgdata/geneseq/geneseq/AA1999.DAT: \*  
22: /SIDSB/gcgdata/geneseq/geneseq/AA2000.DAT: \*  
23: /SIDSB/gcgdata/geneseq/geneseq/AA2001.DAT: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2084	99.7	411	20	AAV28497
2	2044	97.8	411	20	AAV34133
3	2044	97.8	411	20	AAV28496
4	2044	97.8	411	22	AAV50044
5	1864	89.2	370	20	AAV30648
6	797	38.1	393	21	AAV94425
7	797	38.1	393	20	AAV94426
8	770.5	36.9	398	20	AAV30647
9	551	26.4	107	20	AAV28498
10	420	20.1	499	21	AAV90356
11	420	20.1	499	21	AAV96675

12	420	20.1	499	21	AAV94875	Human protein clon
13	392	18.8	361	22	AAV31805	Amino acid sequenc
14	387	18.5	332	21	AAV90354	Human TWIK-3 prote
15	376.5	18.0	336	18	AAV23397	Human TWIK-1 potassiu
16	376.5	18.0	336	21	AAV96673	Human TWIK-1 potassiu
17	370	17.7	394	21	AAV96674	Human TWIK-1 potassiu
18	370	17.7	394	21	AAV96674	Human TWIK-1 potassiu
19	345	16.5	405	21	AAV95230	Human TWIK-1 potassiu
20	342.5	16.4	374	21	AAV18807	Human TWIK-1 potassiu
21	342.5	16.4	374	21	AAV18807	Human TWIK-1 potassiu
22	342	16.4	313	20	AAV34132	Human TWIK-1 potassiu
23	342	16.4	313	20	AAV34132	Human TWIK-1 potassiu
24	342	16.4	313	21	AAV90355	Human TWIK-4 prote
25	342	16.4	313	21	AAV90355	Human TWIK-4 prote
26	342	16.4	313	21	AAV90355	Human TWIK-4 prote
27	317.5	15.2	408	22	AAV8738	Human TWIK-4 prote
28	317.5	15.2	408	22	AAV8738	Human TWIK-4 prote
29	256.5	12.3	395	22	AAV1801	Human TWIK-4 prote
30	219	10.5	336	17	AAV97986	Human TWIK-4 prote
31	216.5	10.4	730	22	AAV1800	Human TWIK-4 prote
32	210.5	10.1	995	22	AAV1799	Human TWIK-4 prote
33	184.5	8.8	383	21	AAV96677	Human TWIK-4 prote
34	172	8.2	1153	22	AAV1802	Human TWIK-4 prote
35	160.5	7.7	347	21	AAV96676	Human TWIK-4 prote
36	152.5	7.3	197	20	AAV34126	Human TWIK-4 prote
37	144.5	6.9	316	21	AAV34160	Human TWIK-4 prote
38	144.5	6.9	316	21	AAV34160	Human TWIK-4 prote
39	144.5	6.9	408	21	AAV34159	Human TWIK-4 prote
40	144.5	6.9	408	21	AAV34159	Human TWIK-4 prote
41	138.5	6.6	248	21	AAV4161	Human TWIK-4 prote
42	138.5	6.6	248	21	AAV4161	Human TWIK-4 prote
43	137.5	6.6	399	21	AAV41831	Human TWIK-4 prote
44	137.5	6.6	424	21	AAV41830	Human TWIK-4 prote
45	137.5	6.6	436	21	AAV41829	Human TWIK-4 prote

#### ALIGNMENTS

RESULT 1  
ID AAV28497 standard; Protein: 411 AA.  
AC AAV28497;  
XX  
XX 12-OCT-1999 (first entry)  
XX  
XX Mouse h-TREK1 polypeptide.  
XX  
XX h-TREK1; two pore potassium channel; inflammatory disease;  
XX chromosome 1q32.  
XX  
XX Mus musculus.  
XX  
XX WO9937762-A1.  
XX  
XX 29-JUL-1999.  
XX  
XX 02-DEC-1998; 98WO-EP07805.  
XX  
XX 09-OCT-1998; 98GB-0022135.  
XX  
XX 27-JAN-1998; 98EP-0300570.  
XX  
XX (SMIK ) SMITHKLINE BEECHAM PLC.  
XX  
XX Chapman CG, Meadows HJ;  
XX  
XX WPI: 1999-469126/39.  
XX  
XX N-PSDB; AA200040.  
XX  
XX New two pore potassium channel used for, e.g. treatment of cancer,  
XX pulmonary, cardiovascular and inflammatory diseases

PS Claim 3; Page 26; 44pp; English.

XX This sequence is the mouse h-TREK1 polypeptide, encoded by the h-TREK1

CC polynucleotide AA00040. h-TREK1 is a two pore potassium channel.

CC The polynucleotide sequence of h-TREK1 can be used to diagnose a

CC disease or susceptibility to a disease related to expression or activity

CC of h-TREK1 polypeptides. The methods of diagnosis may be used in the

CC treatment of diseases including cancer, pulmonary, cardiovascular, and

CC inflammatory diseases, pain, psychiatric disorders including depression

CC and schizophrenia, neurodegenerative diseases including Alzheimer's,

CC stroke, and head trauma and neurological disorders including migraine.

XX

SQ Sequence 411 AA:

Query Match 99.7%; Score 2084; DB 20; Length 411;

Best Local Similarity 99.8%; Pred. No. 1.4e-217;

Matches 410; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAAPDLDPKSAQNSKPRLSFSKRPVLASRVESDSAINVMKKTSTFLVVLII 60

DB 1 maapdlldpkasaqnskpriksfkskprvlarsvesdsainvmkktstflvvllylil 60

QY 61 GAAVFKALEOPQISQRTTIVIOKOTIAQACVNSTELDLIOQIVAAINAGIPLGNS 120

DB 61 gaavfkaleqpgelsqrtlviqkqtliaqhacvnsdelldliqivaainagilplgns 120

QY 121 SNOVSHMDLGSSEFFAGTAVTTTIGFGNISPRTEGKIFCIYVALGIFLPGFLAGVGDQ 180

DB 121 snovshmdlgsseffagvtavtttligfgnisprrteggkifciylvalgflpgflagvgdq 180

QY 181 LGTIFGKGIKVEDTFRKMWVSQTKIRIISTIFILFGCVLPAVPAVIRKHIEGWSALD 240

DB 181 lgtifgkikavedtfrkmvvsqtkiristifilfgcvlpaavirakhiegwsald 240

QY 241 AITFVVTTLTTIGFGDVAGSDIEVDFKPYVWFWIIVGLAFVAVLSMGDMIRVIS 300

DB 241 aifvvtlittligfgdvaggsdievdfkpyvwfwilvlglaavlsmldmrlvis 300

QY 301 KKTKEEYGEFRAHAETAVTAETAEFKTRRRRLSVEIDKFORATSVKRLSAGELAGNHQ 360

DB 301 kktkeeygefrahaetaavtaetaefktrrrrlsveidkforatstvkrksaagelagnhq 360

QY 361 ELTPCRRRTLSVNHUTSREVLPLPLKAESITYLNGLRPHCAGEDIAVIENMK 411

DB 361 eltpcrrtlsvnhltserdlplplkkesiylnglrphcagediaviennk 411

RESULT 2

AA034133 ID AA034133 standard; Protein; 411 AA.

AC AA034133:

XX 30-NOV-1999 (first entry)

DE Human potassium channel K+Hnov59.

XX

KM Potassium channel; ataxia; arrhythmia; epilepsy; Bartter's syndrome;

KW cardiovascular disorder; CNS disorder; renal disorder.

XX

OS Homo sapiens.

XX

PN MO9943696-AI.

XX

PD 02-SEP-1999.

XX

PF 22-FEB-1999; 99MO-US03826.

XX

PR 19-JAN-1999; 99US-0116448.

PR 25-FEB-1998; 98US-0076687.

PR 07-AUG-1998; 98US-0095836.

XX

PA (AXYS-) AXYS PHARM INC.

XX

PI Curran ME, Hu P, Miller AP, Rutter M, Wang J;

XX WPI, 1999-527591/44.

DR N-PSDB; AA211915.

XX

XX New nucleic acids encoding mammalian K+Hnov potassium channel

PT proteins, useful for the diagnosis and treatment of episodic ataxia

PT with myokymia, cardiac arrhythmia, epilepsy and Bartter's syndrome

XX

PS Claim 3; Page 104-105; 112pp; English.

XX

XX This sequence represents the human K+Hnov59 potassium channel.

CC K+Hnov proteins have a high degree of homology to known potassium

CC channels and may be alpha subunits, which form the functional channel,

CC or accessory subunits that act to modulate the channel activity. K+Hnov59

CC is a 4 transmembrane domain, 2 pore domain potassium channel. The gene

CC is located on chromosome 19, determined via 3C chromosomes

CC localisation using primers AA211939 and AA211940. K+Hnov cDNAs

CC were isolated by extension of expressed sequence tags (ESTs) which were

CC related but not identical to known human potassium channels. Potential

CC polymorphisms detected as sequence variants between multiple

CC independent clones. Potassium channels have critical roles in various

CC cell types and biochemical pathways. Defective potassium channels are

CC known to cause four human diseases: episodic ataxia with myokymia;

CC cardiac arrhythmia (long QT syndrome); epilepsy; and Bartter's syndrome.

CC As potassium channels are critical components of virtually all cells,

CC it is likely that abnormal potassium channels are also implicated in

CC certain renal, cardiovascular and central nervous system (CNS)

CC disorders. Nucleotides encoding K+Hnov proteins may be used for

CC identifying homologous or related proteins and the DNA sequences encoding

CC them. They may be used to produce compositions that modulate the

CC expression and function of the K+Hnov protein and in studying the

CC biochemical pathways associated with it. They may also be used for the

CC recombinant production of K+Hnov protein in fermentation cultures.

CC Additionally, such nucleotides may be used in gene therapy protocols for

CC the treatment of diseases associated with abnormal potassium channels.

XX

SQ Sequence 411 AA:

Query Match 97.8%; Score 2044; DB 20; Length 411;

Best Local Similarity 96.4%; Pred. No. 3.1e-213;

Matches 396; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

QY 1 MAAPDLDPKSAQNSKPRLSFSKRPVLASRVESDSAINVMKKTSTFLVVLII 60

DB 1 maapdlldpkasaqnskpriksfkskprvlarsvesdsainvmkktstflvvllylil 60

QY 61 GAAVFKALEOPQISQRTTIVIOKOTIAQACVNSTELDLIOQIVAAINAGIPLGNS 120

DB 61 gaavfkaleqpgelsqrtlviqkqtliaqhacvnsdelldliqivaainagilplgns 120

QY 121 SNOVSHMDLGSSEFFAGTAVTTTIGFGNISPRTEGKIFCIYVALGIFLPGFLAGVGDQ 180

DB 121 snovshmdlgsseffagvtavtttligfgnisprrteggkifciylvalgflpgflagvgdq 180

QY 181 LGTIFGKGIKVEDTFRKMWVSQTKIRIISTIFILFGCVLPAVPAVIRKHIEGWSALD 240

DB 181 lgtifgkikavedtfrkmvvsqtkiristifilfgcvlpaavirakhiegwsald 240

QY 241 AITFVVTTLTTIGFGDVAGSDIEVDFKPYVWFWIIVGLAFVAVLSMGDMIRVIS 300

DB 241 aifvvtlittligfgdvaggsdievdfkpyvwfwilvlglaavlsmldmrlvis 300

QY 301 KKTKEEYGEFRAHAETAVTAETAEFKTRRRRLSVEIYD...ATSVKRLSAGELAGNHQ 360

DB 301 kktkeeygefrahaetaavtaetaefktrrrrlsveiyd...atsvkrksaagelagnhq 360

QY 361 ELTPCRRRTLSVNHUTSREVLPLPLKAESITYLNGLRPHCAGEDIAVIENMK 411

DB 361 eltpcrrtlsvnhltserdlplplkkesiylnglrphcagediaviennk 411

```

RESULT 3
AAV28496
ID AAV28496 standard; Protein; 411 AA.
XX
AC AAV28496;
XX
DT 12-OCT-1999 (first entry)
XX
DE h-TREK1 polypeptide.
XX
KM h-TREK1; two pore potassium channel; inflammatory disease;
XX chromosome 1q32.
XX
OS Homo sapiens.
XX
PN MO9937762-A1.
XX
PD 29-JUL-1999.
XX
PF 02-DEC-1998; 98MO-EP07805.
XX
PR 09-OCT-1998; 98GB-0022135.
XX
PR 27-JAN-1998; 98EP-0300570.
XX
PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI Chapman CG, Meadows HJ;
XX
DR WPI; 1999-469126/39.
XX
DR N-PSDB; AAZ00039.
XX
PT New two pore potassium channel used for, e.g. treatment of cancer,
XX pulmonary, cardiovascular and inflammatory diseases
XX
Claim 3; Page 24; 44pp; English.
XX
XX
XX This sequence is the h-TREK1 polypeptide, encoded by the h-TREK1
XX polynucleotide AAZ00039. h-TREK1 is a two pore potassium channel, and
XX the gene maps to human chromosome 1q32, between the markers DIS237 and
XX W5105. The polynucleotide sequence of h-TREK1 can be used to diagnose a
XX disease or susceptibility to a disease related to expression or activity
XX of h-TREK1 polypeptides. The methods of diagnosis may be used in the
XX treatment of diseases including cancer, pulmonary, cardiovascular, and
XX inflammatory diseases, pain, psychiatric disorders including depression
XX and schizophrenia, neurodegenerative diseases including Alzheimer's,
XX stroke, and head trauma and neurological disorders including migraine.
XX
SQ Sequence 411 AA;

Query Match 97.8%; Score 2044; DB 20; Length 411;
Best Local Similarity 96.4%; Pred. No. 3.1e-213;
Matches 396; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

OY 1 MAAPDLDPKSAONSKPRLSFSKPTVLASRVESDAINVMKKTSTIFLVVVLII 60
DB 1 maepdlldpksaonksprlsfskptvlasrvesdai nvmkktstiflvvvl i 60
OY 61 GAAVKALEQPOEISQRTTIVIKQFIAOHCACVNSTEDELDOOIVAAINAGIPLGNS 120
DB 61 gaa vka leq poe is q r t t i v i k q f i a o h c a c v n s t e d e l d o o i v a a i n a g i p l g n s 120
OY 121 SNOVSHMDLGSSFFACTVITTTGFGNISPRTEGKIFCIITIALGLPRLGFLAGVGDQ 180
DB 121 snovshmdlgssffactvitttgfgn isprte gk ifci itia lglp rlg flag vgdq 180
OY 181 LGTFGKGIAKVEDTFFIKMNVNOSKIRIISITFIIFGCVLFVALPVIFPHIGMSALD 240
DB 181 l g t f g k g i a k v e d t f f i k m n v n o s k i r i i s i t f i i f g c v l f v a l p v i f p h i g m s a l d 240
OY 241 AIYFVITLTATIGRGDYVAGSDIEYLDFFYKPVVMFVLGLAVFAAVLSMIGMLRVIS 300
DB 241 ai y f v i t l t a t i g r g d y v a g s d i e y l d f f y k p v v m f v l g l a v f a a v l s m i g m l r v i s 300

```

```

RESULT 4
AAB50044
ID AAB50044 standard; Protein; 411 AA.
XX
AC AAB50044;
XX
DT 19-MAR-2001 (first entry)
XX
DE Human TREK.
XX
KM Human; TREK: 2p domain potassium channel; re-l 9 membrane potential;
XX neuronal excitability; neurotransmitter releas modulation; epilepsy;
XX neurological disorder; sleep-related disorder; cognitive dysfunction;
XX attention deficit disorder; addiction; anxiety; phobia;
XX Parkinson's chorea; Huntington's chorea; cereb at palsy; Incontinence;
XX erectile dysfunction; alopecia.
XX
OS Homo sapiens.
XX
PN MO200072863-A2.
XX
PD 07-DEC-2000.
XX
PE 01-JUN-2000; 2000MO-GE02107.
XX
PR 01-JUN-1999; 99GB-0012733.
XX
PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI Hervieu GJ, Meadows HJ, Randall AD;
XX
DR WPI; 2001-080422/09.
XX
DR N-PSDB; AAC90412.
XX
PT Use of human TREK1 polypeptide, polynucleo encoding them and
XX modulators of h-TREK1 polypeptides for treating epilepsy, sleep-related
XX disorders, addiction and dyskinesias including Parkinson's and
XX Huntington's chorea
XX
PS Claim 7; Page 29; 35pp; English.
XX
XX
XX The present sequence is human TREK1 (h-TREK1). h-TREK1 is a member of the
XX 2p domain potassium channel family of proteins, which play a part in the
XX control of resting neuronal membrane potential. Modulation of these channels will
XX therefore affect neuronal excitability, thereby leading to a modulation
XX of neurotransmitter release and activity of neuronal networks. Such
XX modulation therefore may be useful for the treatment of certain
XX neurological conditions such as epilepsy, sleep-related disorders,
XX cognitive dysfunction, attention deficit disorder, anxiety, addiction,
XX anxiety/phobia, Parkinson's and Huntington's chorea, cerebral palsy,
XX incontinence, erectile dysfunction or alopecia.
XX
SQ Sequence 411 AA;

Query Match 97.8%; Score 2044; DB 20; Length 411;
Best Local Similarity 96.4%; Pred. No. 3.1e-213;
Matches 396; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

OY 1 MAAPDLDPKSAONSKPRLSFSKPTVLASRVESDAINVMKKTSTIFLVVVLII 60
DB 1 maepdlldpksaonksprlsfskptvlasrvesdai nvmkktstiflvvvl i 60

```

Db 1 maapdlldpksaagnskprlsfskptvlasrvesdcltnvmkwtvstflvvlylil 60  
 QY 61 GAAVFALDQPOEISORTITIVIOKOTFIQAOHACVNSTEDELIOQIVAAINAGIPLGNS 120  
 Db 61 gatvfakaleqpeisqrtlivlqkqtlfiqhsqscvnsteldelidqlvaainagilplgnt 120  
 QY 121 SNOVSHMDLGSSFFEFAGVTITTTIGFNGNISPRTEGKIFCIYALLGIPLEGFLACVGDO 180  
 Db 121 snqshmdlgssffefagvtitltigfnisprteggkifcilyallgiplegflagvgdq 180  
 QY 181 LGTIFGKGIKAVEDTPEIKNNVSQTKIRIISTIFILFGCVLPALPAVIFKHIEGNSALD 240  
 Db 181 lgtifgkgiakavedtpeiknnvsqtkiristifilfgcvlpalpaavifkhiegsald 240  
 QY 241 AIFYFVITTTTIGFGDYVAGSDIEYLDYKPPYWMFIIWGLAFPAVLSMIGDMLRVIS 300  
 Db 241 aifyfvitltitigfdyvaggsdieyldfykppvwfllwglayfaavlsmgldwlrvis 300  
 QY 301 KTKKEEVGEFRAHAEMWTANVTAEFKETRRLRSVEIYDKFQRTSVKRLSALAGNHQ 360  
 Db 301 ktkkeevgefrahhaemwtanvtaefketrirlsveliydkfqratsvkrksaelagnhq 360  
 QY 361 ELTPCRRITSVNHLTSEREVLPPILKAESTYINGLTPHAGEDIATVENMK 411  
 Db 361 eltpcrritlvnhltserevlppllkastyingltphagaeiatvenmk 411

## RESULT 5

AA930648  
 ID AAY30648 standard. Protein: 370 AA.

AA930648;

18-NOV-1999 (first entry)

A mechanically sensitive potassium channel protein TREK-1.

XX Mechanically sensitive potassium channel protein: TREK-1;  
 KW polyunsaturated fatty acid; arachidonic acid; riluzole; heart disease;  
 KW nervous system disease; epilepsy; cardiovascular disease; arrhythmia;  
 KW neurodegeneration; ischemia; anoxia; hormone secretion abnormality;  
 KW muscular disease.

XX Mus sp.

XX WO9945108-A2.

XX 10-SEP-1999.

XX 23-FEB-1999; 99WO-FR00404.

XX 05-MAR-1998; 98FR-0002725.

XX (CNRS ) CNRS CENT NAT RECH SCI.

XX Honore E, Fink M, Lazdunski M, Lesage F, Duprat F;

XX WPI: 1999-551038/46.

XX N-PSDB: AA210607.

XX New mechanically sensitive potassium channel, used to screen for  
 PT specific modulators, potential therapeutic agents for heart and nervous  
 PT system disorders

XX Claim 3; Page 23-25; 40pp; French.

XX The present sequence represents a mechanically sensitive potassium  
 CC channel protein designated TREK-1. The protein is activated by  
 CC polyunsaturated fatty acids, particularly arachidonic acid, and by  
 CC riluzole. The protein is used to screen for specific modulators which  
 CC are useful for treating or preventing diseases of the heart and nervous  
 CC systems in humans and animals, e.g. epilepsy, cardiovascular disease  
 CC (arrhythmia), neurodegeneration (particularly where associated with

CC ischemia or anoxia), abnormalities of hormone secretion and muscular  
 CC disease. The protein itself may be used to treat these diseases.  
 CC Antibodies specific for the protein are used to detect it in tissues,  
 CC also as therapeutic inhibitors or activators.

XX Sequence 370 AA:

Query Match 89.2%; Score 1864; D: Length 370;  
 Best Local Similarity 99.7%; Pred. No. 9.3e Indels 0; Gaps 0;  
 Matches 367; Conservative 0; Mismatches

QY 1 MAAPDLDPKSAAGNSKPRLSFSKPTVLAARVESDSA 60  
 Db 1 maapdlldpksaagnskprlsfskptvlasrvesdsa 60  
 QY 61 GAAVFALDQPOEISORTITIVIOKOTFIQAOHACVNSTE 120  
 Db 61 gaavfaleqpeisqrtlivlqkqtlfiqhsqscvnsteldelidqlvaainagilplgns 120  
 QY 121 SNOVSHMDLGSSFFEFAGVTITTTIGFNGNISPRTEGKIF 180  
 Db 121 snqshmdlgssffefagvtitltigfnisprteggkifcilyallgiplegflagvgdq 180  
 QY 181 LGTIFGKGIKAVEDTPEIKNNVSQTKIRIISTIFILFGCVLPALPAVIFKHIEGNSALD 240  
 Db 181 lgtifgkgiakavedtpeiknnvsqtkiristifilfgcvlpalpaavifkhiegsald 240  
 QY 241 AIFYFVITTTTIGFGDYVAGSDIEYLDYKPPYWMFIIWGLAFPAVLSMIGDMLRVIS 300  
 Db 241 aifyfvitltitigfdyvaggsdieyldfykppvwfllwglayfaavlsmgldwlrvis 300  
 QY 301 KTKKEEVGEFRAHAEMWTANVTAEFKETRRLRSVEIYDKFQRTSVKRLSALAGNHQ 360  
 Db 301 ktkkeevgefrahhaemwtanvtaefketrirlsveliydkfqratsvkrksaelagnhq 360  
 QY 361 ELTPCRRITSVNHLTSEREVLPPILKAESTYINGLTPHAGEDIATVENMK 411  
 Db 361 eltpcrritlvnhltserevlppllkastyingltphagaeiatvenmk 411

## RESULT 6

AA94425  
 ID AAY94425 standard. Protein: 393 AA.

AA94425;

04-AUG-2000 (first entry)

XX Human h-TRAK polypeptide #1.

XX Human; h-TRAK; potassium channel polypeptide; disease: stroke;

XX 2P domain potassium channel; neurodegenerative therapy.

XX Homo sapiens.

XX WO200026253-A1.

XX 11-MAY-2000.

XX 03-NOV-1999; 99WO-GB03634.

XX 03-NOV-1998; 98GB-0024048.

XX 07-OCT-1999; 99GB-0023668.

XX (SMK ) SMITHKLINE BEECHAM PLC.

XX Chapman CG, Duckworth DM;

XX WPI: 2000-365583/31.

XX N-PSDB: AAA27105.



PT Novel isolated h-TRAAK polypeptides belonging to the potassium channel  
PT family of polypeptides, useful for the diagnosis and treatment of  
PT h-TRAAK related disorders, e.g. depression and schizophrenia -  
XX  
XX  
PS Claim 3; Page 21; 35pp; English.  
XX  
CC Functional genomics was used to identify h-TRAAK polypeptides and  
CC h-TRAAK polynucleotides from human tissue samples. h-TRAAK  
CC polypeptides have homology to the 2P domain potassium channel family of  
CC polypeptides. The h-TRAAK polypeptides and polynucleotides may  
CC be used in diagnostic assays for conditions related to h-TRAAK  
CC imbalance and for identifying agonists and antagonists of h-TRAAK  
CC polypeptides. The h-TRAAK polypeptides and polynucleotides may also  
CC be useful for treatment and prevention (e.g. as vaccines) of certain  
CC diseases, such as pain, psychiatric disorders including depression and  
CC schizophrenia, neurodegenerative disease including Alzheimer's, stroke  
CC and head trauma and neurological disorders including migraine and  
CC epilepsy. The present sequence is human h-TRAAK protein #1.  
XX  
SQ Sequence 393 AA;  
XX  
Query Match 38.1%; Score 797; DB 21; Length 393;  
Best Local Similarity 51.1%; Pred. No. 7.5e-78;  
Matches 145; Conservative 60; Mismatches 77; Indels 2; Gaps 1;  
OY 42 MKMKVSTIFLVVLYLIGAAVFAKLEPOEISORTIVIKQFIFQAHCVNSTEIDE 101  
DB 1 mstlllaialvallylvgalvralaqneqgeqreigevreflrahpsvdsqelgl 60  
OY 102 LIQOIQAIAINAGIIPLGSSNOVSH-WDLGSSFEFFACTVTTTIGFNGISPRTEGKIFC 159  
DB 61 lkevadalgsgadepetnssnshsawdlgsaffsglttltygvalrtdegrlfc 120  
OY 160 IYVALGTPLEGFLLAGGDDQGTIFGKIGAKVEPTFKKAVNSQKRIITSTIIFILEGC 219  
DB 121 lfyalvgiprlglllagvdrigsrlrhylghlealflkwnvpelvtvsamfillllygc 180  
OY 220 VLFAVLPVIRFKHIEGMSALDAIYFVVTTLTIGFGDYVAGSDIEYDFKPVVWFIL 279  
DB 181 llfvlprfvcymedwskleaiyfvivltltvfgdyvvaqadprqdsapayqplwfwll 240  
OY 280 VGLAVFAVLSMIGDMLRVISKTKKEVEGFRRAHAEMTAVNTA 323  
DB 241 lglayfasvltlctlgmwlrvsrrtraemgyltaqaaswtgcvta 284  
RESULT 7  
AAV94426  
ID AAV94426 standard; Protein; 393 AA.  
XX  
XX AAV94426;  
AC  
XX  
DT 04-AUG-2000 (first entry)  
XX  
DE Human h-TRAAK polypeptide #2.  
XX  
KW Human: h-TRAAK: potassium channel polypeptide;  
KW 2P domain potassium channel; neurodegenerative disease; stroke;  
KW psychiatric disorder; neurological disorder; Gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN WC0200026253-A1.  
PD 11-MAY-2000.  
XX  
PE 03-NOV-1999; 99WO-GB03634.  
XX  
PR 03-NOV-1998; 98GB-0024048.  
PR 07-OCT-1999; 99GB-0023668.  
XX  
PA (SMIK ) SMITHKLINE BEECHAM PLC.

XX  
PI Chapman CG, Duckworth DM;  
XX  
XX WPI: 2000-365583/31.  
DR N-PSDB: AAA27106.  
XX  
PT Novel isolated h-TRAAK polypeptides belonging to the potassium channel  
PT family of polypeptides, useful for the diagnosis and treatment of  
PT h-TRAAK related disorders, e.g. depression and schizophrenia -  
XX  
XX  
PS Claim 12; Pages 21 and 22; 35pp; English.  
XX  
CC Functional genomics was used to identify h-TRAAK polypeptides and  
CC h-TRAAK polynucleotides from human tissue samples. h-TRAAK  
CC polypeptides have homology to the 2P domain potassium channel family of  
CC polypeptides. The h-TRAAK polypeptides and polynucleotides may  
CC be used in diagnostic assays for conditions related to h-TRAAK  
CC imbalance and for identifying agonists and antagonists of h-TRAAK  
CC polypeptides. The h-TRAAK polypeptides and polynucleotides may also  
CC be useful for treatment and prevention (e.g. as vaccines) of certain  
CC diseases, such as pain, psychiatric disorders including depression and  
CC schizophrenia, neurodegenerative disease including Alzheimer's, stroke  
CC and head trauma and neurological disorders including migraine and  
CC epilepsy. The present sequence is human h-TRAAK protein #2.  
XX  
SQ Sequence 393 AA;  
XX  
Query Match 38.1%; Score 797; DB 21; Length 393;  
Best Local Similarity 51.1%; Pred. No. 7.5e-78;  
Matches 145; Conservative 60; Mismatches 77; Indels 2; Gaps 1;  
OY 42 MKMKVSTIFLVVLYLIGAAVFAKLEPOEISORTIVIKQFIFQAHCVNSTEIDE 101  
DB 1 mstlllaialvallylvgalvralaqneqgeqreigevreflrahpsvdsqelgl 60  
OY 102 LIQOIQAIAINAGIIPLGSSNOVSH-WDLGSSFEFFACTVTTTIGFNGISPRTEGKIFC 159  
DB 61 lkevadalgsgadepetnssnshsawdlgsaffsglttltygvalrtdegrlfc 120  
OY 160 IYVALGTPLEGFLLAGGDDQGTIFGKIGAKVEPTFKKAVNSQKRIITSTIIFILEGC 219  
DB 121 lfyalvgiprlglllagvdrigsrlrhylghlealflkwnvpelvtvsamfillllygc 180  
OY 220 VLFAVLPVIRFKHIEGMSALDAIYFVVTTLTIGFGDYVAGSDIEYDFKPVVWFIL 279  
DB 181 llfvlprfvcymedwskleaiyfvivltltvfgdyvvaqadprqdsapayqplwfwll 240  
OY 280 VGLAVFAVLSMIGDMLRVISKTKKEVEGFRRAHAEMTAVNTA 323  
DB 241 lglayfasvltlctlgmwlrvsrrtraemgyltaqaaswtgcvta 284  
RESULT 8  
AAV30647  
ID AAV30647 standard; Protein; 398 AA.  
XX  
XX AAV30647;  
AC  
XX  
DT 18-NOV-1999 (first entry)  
XX  
DE A mechanically sensitive potassium channel protein TRAAK.  
XX  
KW Mechanically sensitive potassium channel protein; TRAAK;  
KW polyunsaturated fatty acid; arachidonic acid; filizole; heart disease;  
KW nervous system disease; epilepsy; cardiovascular disease; arrhythmia;  
KW neurodegeneration; ischemia; anoxia; hormone secretion abnormality;  
KW muscular disease.  
XX  
OS Mus sp.  
XX  
PN WO9945108-A2.

PD 10-SEP-1999.  
 XX 23-FEB-1999; 99WO-FR00404.  
 XX 05-MAR-1998; 98FR-0002725.  
 XX (CNRS ) CNRS CENT NAT RECH SCI.  
 XX PA  
 XX PI Honore E, Fink M, Lazdunski M, Lesage F, Duprat F;  
 XX DR MPI: 1999-551038/46.  
 XX DB N-PSDB; AA210606.  
 PT New mechanically sensitive potassium channel, used to screen for  
 PT specific modulators, potential therapeutic agents for heart and nervous  
 PT system disorders  
 XX  
 PS Claim 2: Fig 1: 40pp; French.  
 CC The present sequence represents a mechanically sensitive potassium  
 CC channel protein designated TRAK. The protein is activated by  
 CC polyunsaturated fatty acids, particularly arachidonic acid, and by  
 CC riluzole. The protein is used to screen for specific modulators which  
 CC are useful for treating or preventing diseases of the heart and nervous  
 CC systems in humans and animals, e.g. epilepsy, cardiovascular disease  
 CC (arrhythmia), neurodegeneration (particularly where associated with  
 CC ischemia or anoxia), abnormalities of hormone secretion and muscular  
 CC disease. The protein itself may be used to treat these diseases.  
 CC Antibodies specific for the protein are used to detect it in tissues,  
 CC also as therapeutic inhibitors or activators.  
 XX  
 SQ Sequence 398 AA;  
 XX  
 Query Match 36.9%; Score 770.5; DB 20: Length 398;  
 Best Local Similarity 49.8%; Pred. No. 5.8e-75;  
 Matches 142; Conservative 56; Mismatches 84; Indels 3; Gaps 1;  
 QY 42 MKRKTSTFLVVLVLLIGAAVFKALEPQETISQRTTIVIOKQTFIAOHACVNSTELDE 101  
 DB 1 msttllallalvllvlgslvfgaleqhegqackkmdhgdqfirdpcvsqskled 60  
 QY 102 LIOQIVAAINAGIIP--LGNSSNOVSHMDLGSSFFPAGTIVITIGNISPTEGGKIF 158  
 DB 61 fklrlvealggnanpetswcnssnhsaamlgsaffsgltitlgynlvtldagrlf 120  
 QY 159 CIYALGIPFLGFGFLAGVDGLGTFKGIARVEDPFIKWNVSQTKIRIRISTITFLFG 218  
 DB 121 cllfyalvlgplfgmllagvadrfgslrrgldhealfkwhvppglvrlsavllflig 180  
 QY 219 CVLEVALPAVIFKRIHGSWALDAIYEVVITLTIGFGDYVAGSDIEYLDYKPVVFWI 278  
 DB 181 cllfvltpftfsvmeswsllealfytlvtlvtgfdyppgdtgtnspayglvfwfwi 240  
 QY 279 LVGLATFAAVLSMIGDMLRYSKTKKEEGEGRHAHAETANTYA 323  
 DB 241 llglayfasvlticglnwlravsrtrraemgylagaaswtgltvla 285  
 RESULT 9  
 AAAY28498  
 ID AAY28498 standard; Protein; 107 AA.  
 XX  
 AC AAY28498;  
 XX  
 DT 12-OCT-1999 (first entry)  
 XX  
 DE Partial h-TREK1 polypeptide.  
 XX  
 KW partial h-TREK1: two pore potassium channel; inflammatory disease;  
 KW chromosome 1q32.  
 XX  
 OS Homo sapiens.

XX Key Location/Qualifiers  
 FH Misc-difference 2 /note= "Encoded by ACC"  
 FT FT  
 FT Misc-difference 6 /note= "Encoded by CAA"  
 FT FT  
 XX MO937762-A1.  
 XX  
 XX 29-JUL-1999.  
 XX  
 XX 02-DEC-1998; 98WO-EP07805.  
 XX  
 XX 09-OCT-1998; 98GB-0022135.  
 XX PR 27-JAN-1998; 98EP-0300570.  
 XX  
 XX (SMK ) SMITHKLINE BEECHAM PLC.  
 XX  
 XX Chapman CG, Meadows HJ;  
 XX PI  
 XX DR MPI: 1999-469126/39.  
 XX DB N-PSDB; AA200041.  
 PT New two pore potassium channel used for, e.g. treatment of cancer,  
 PT pulmonary, cardiovascular and inflammatory diseases  
 XX  
 PS Claim 18; Page 25; 44pp; English.  
 CC This sequence is a partial h-TREK1 polypeptide encoded by the h-TREK1  
 CC polynucleotide AA200041. AA200039 and AAY28498 are complete h-TREK1  
 CC polynucleotide and polypeptide sequences. h-TREK1 is a two pore  
 CC potassium channel, and the gene maps to human chromosome 1q32, between  
 CC the markers DIS237 and W15105. The polynucleotide sequence of h-TREK1 can  
 CC be used to diagnose a disease or susceptibility to a disease related to  
 CC expression or activity of h-TREK1 polypeptide. The methods of diagnosis  
 CC may be used in the treatment of diseases including cancer, pulmonary,  
 CC cardiovascular, and inflammatory diseases, psychiatric disorders  
 CC including Alzheimer's, stroke, and head trauma and neurological  
 CC disorders including migraine.  
 XX  
 SQ Sequence 107 AA;  
 XX  
 Query Match 26.4%; Score 551; DE 20: Length 107;  
 Best Local Similarity 100.0%; Pred. No. 5.7e-71;  
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 119 NSSNOVSHMDLGSSFFPAGTIVITIGGNISPTEGGKIF 178  
 DB 1 nssnqshwldlgssffagvtltitlgfnisprteggkifcylallgplfgllagvg 60  
 QY 179 DQIGTFKGIARVEDPFIKWNVSQTKIRIRISTITFL 225  
 DB 61 dqigltfkgkrlavedfllkwnvsqtkiristitflilcvlval 107  
 RESULT 10  
 AAAY90356  
 ID AAY90356 standard; Protein; 499 AA.  
 XX  
 AC AAY90356;  
 XX  
 DT 04-DEC-2000 (first entry)  
 XX  
 DE Human TWIK-2 protein.  
 XX  
 KW Human; TWIK-3; TWIK-4; TWIK-2; central nervous system disorder; dementia;  
 KW Tandem of P domains in a weak inward rectifying K<sup>+</sup> channel; epilepsy;  
 KW Alzheimer's disease; Parkinson's disease; multiple sclerosis; depression;  
 KW amyotrophic lateral sclerosis; progressive supranuclear palsy; mania;  
 KW Creutzfeldt-Jacob disease; psychiatric disorder; schizophrenic disorder;  
 KW Korsakoff's psychosis; anxiety disorder; phobic disorder; amnesia;  
 KW







CC This sequence represents the human TWIK-3 protein of the invention. The  
 CC TWIK-2 (Tandem of P domains in a Weak Inward rectifying potassium (K<sup>+</sup>)  
 CC channel-2), TWIK-3 and TWIK-4 nucleic acids and proteins are useful as  
 CC targets for developing modulating agents to regulate a variety of  
 CC cellular processes. They may be useful for developing novel diagnostic  
 CC and therapeutic agents for potassium channel associated disorders,  
 CC e.g. central nervous system disorders (e.g. Alzheimer's disease,  
 CC dementia, Parkinson's disease, multiple sclerosis, amyotrophic lateral  
 CC sclerosis, progressive supranuclear palsy, epilepsy, Creutzfeldt-Jacob  
 CC disease), psychiatric disorders (e.g. depression, schizophrenia,  
 CC disorders, Korsakoff's psychosis, mania, anxiety disorders or phobic  
 CC disorders), learning or memory disorders (e.g. amnesia or age-related  
 CC memory loss), neurological disorders (e.g. migraine), obesity, and  
 CC cardiac disorders. The nucleic acids, proteins, protein homologues and  
 CC antibodies against them may be further used in screening assays,  
 CC predictive medicine. The nucleic acids can be inserted into vectors and  
 CC used as gene therapy vectors, to express TWIK protein, to detect TWIK  
 CC mRNA, modulate TWIK activity, and screen for drugs or compounds that  
 CC modulate TWIK activity. Host cells may be used to produce non-human  
 CC transgenic animals.

CC  
 XX  
 SQ Sequence 332 AA:

Query Match 18.5%; Score 387; DB 21; Length 332;  
 Best Local Similarity 35.5%; Pred. No. 2e-33;  
 Matches 88; Conservative 51; Mismatches 95; Indels 14; Gaps 6;

QY 50 ILVVLVYLIGAAVFAKALPOEISORTTIVIOKQTFINOHACVNSTEDELIOQIVAA 109  
 Db 25 ILIAYLALYLGIVGIVLWLGRAAQDSRSFGQDKWELIGNFCIDLPALDSILRDVQA 84

QY 110 INAGIIPLGSSNOVSHMDGSSFFAGVTITIGFNGISPRTEGGKIFCIITVALGIP 169  
 Db 85 YKGAASLNTTS-MAGVELVGSFFISVSTLTIGYNLSPNCAAILFCIFALYGIPL 143

QY 170 FGFLAGVGQDLGTIEGKI---AKVEDTFIKMNSQTRIRIITIIIFLPGCVLFVAL 225  
 Db 144 NLVL---DRIQLMGQGVNHWASRIQGT---WQ-DPKARVLAGSGLISGLII 195

QY 226 PAVIFKHEGMSALDAIFVYVITLTIGFGDYVAGSDIE-YLDFYPPVWFWILVGLAY 284  
 Db 196 PPIIFSHMWSYLEGYFAFLISTVIGDYVIGMPSQIRPLWYKMNVSILWIIIGMAW 255

QY 285 FAAVLSMI 292  
 Db 256 IALLIKLI 263

RESULT 15

AAM23397  
 ID AAM23397 standard; Protein; 336 AA.

XX  
 AC AAM23397;

XX  
 DT 17-MAR-1998 (first entry)

XX  
 DE TWIK-1 potassium channel protein.

XX  
 KW TWIK-1 potassium channel; screening; diagnosis; transgenic animal;  
 XX Tandem of P domains in a weak inward rectifying K<sup>+</sup> antibody.

OS Homo sapiens.

XX  
 PN FR2744730-A1.

XX  
 PD 14-AUG-1997.

XX  
 PF 08-FEB-1996; 96FR-0001565.

XX  
 PR 08-FEB-1996; 96FR-0001565.

XX  
 PA (CNRS ) CNRS CENT NAT RECH SCI.

XX  
 PI Barhanin J, Duprat F, Fink M, Guillemare E, Lazdunski M;  
 PI Lesage F, Romey G;  
 XX  
 DR WPI, 1997-42773/40.  
 DR N-PSDB; AAT64960.

PT Nucleic acid encoding new potassium channel designated TWIK-1 -  
 PT useful for treating channel deficiency diseases, screening for  
 PT active agents and for diagnosis

PS Claim 12: Figure 1b; 37pp: French.

CC The present sequence represents a protein consisting a potassium channel  
 CC with the properties of a TWIK (Tandem of P domains in a Weak Inward  
 CC rectifying K<sup>+</sup>-1 channel. This is the first member of a new family of  
 CC channels consisting of 4 transmembrane segments and two P domains, and  
 CC being only weakly rectifying. The cDNA, vector, the cells expressing  
 CC TWIK-1 type channels and the protein are used to compensate  
 CC for deficiency of potassium channels in various tissues. Compounds  
 CC for modulating activity of TWIK-1 type channels may also be useful  
 CC therapeutically, e.g. for control of epilepsy, arrhythmia, vascular  
 CC disease, neurodegeneration (particularly of ischemic or anoxic origin),  
 CC endocrine or muscular disorders. The cDNA and the vectors can also be  
 CC used to create transgenic animals (especially knock-out animals) for use  
 CC as models of TWIK-1 related diseases. Analysis of the sequence of the  
 CC TWIK-1 gene may be used for pre-natal diagnosis of disease. Antibodies  
 CC can be used to detect TWIK-1 channels and for inhibiting or activating  
 CC the channels in vivo.

CC  
 XX  
 SQ Sequence 336 AA:

Query Match 18.0%; Score 376.5; DB 18; Length 336;  
 Best Local Similarity 32.5%; Pred. No. 2.8e-32;  
 Matches 90; Conservative 62; Mismatches 104; Indels 17; Gaps 9;

QY 51 FLVV---VLYLIIIGAAVFAKALPOEISORTTIVIOKQTFINACVNSTEDELIOQIVAA 108  
 Db 25 FLVLYLIIYLVFAVVSVELPYEDLIRGELKIKRIFLEECISEGQLEGLISRYVE 84

QY 109 AINAGIIPLGSSNOVSHMDGSSFFAGVTITIGFNGISPRTEGGKIFCIITVALGIP 168  
 Db 85 ASNYGVSVLSNAGN-WNDIFSLASTVISTIGYHLYISDYGKAFCLISVIGIP 143

QY 169 LFGFLAGVGQDLGTIEGKIADVEDTFIKMNSQTRIRIITIIIFLPGCVLFVALP 226  
 Db 144 FCLIFLAVVGRITVHTR--RPVLYFHLIRGFSKQVVAL--NVLIGFVSCFFI--P 199

QY 227 AVIEKHIE-GMSALDAIFVYVITLTIGFGDYVAG-GSDI--LDYKPPVWFWILVGLAY 284  
 Db 200 AAVFSVLDDWFLIESFYCLISLISLIGDYVPGSGYKIKRELKIGITCYLIIIGLIA 259

QY 285 FAAVLSMIGDMLRVISK-----KTKEEVGEFRAHAAB 316  
 Db 260 MLVLETFCE-IHELKFKFMFYVKKKDEDGYHILE 295

Search completed: August 28, 2001, 17:05:47  
 Job time: 1892 sec



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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 28, 2001, 17:06:21 ; Search time 28.01 Seconds  
(without alignments)  
302.129 Million cell updates/sec

Title: US-09-503-089a-4

Perfect score: 2090  
Sequence: 1 MAAPDLDPKSAONSKPRL.....INGLPHCAGEDIAVIENKK 411

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 197339 segs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep.\*  
2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep.\*  
3: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep.\*  
4: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep.\*  
5: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep.\*  
6: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2084	99.7	411	4	US-09-236-080-6
2	2044	97.8	411	4	US-09-236-080-2
3	551	26.4	107	4	US-09-236-080-4
4	376.5	18.0	336	3	US-08-749-816-2
5	299.5	10.5	618	1	US-08-332-312-2
6	219	10.5	336	1	US-08-332-312-4
7	184.5	8.8	383	3	US-08-749-816-4
8	160.5	7.7	347	3	US-08-749-816-3
9	119	5.7	676	4	US-09-135-021-2
10	106.5	5.1	581	4	US-09-135-021-80
11	101.5	4.9	831	2	US-08-677-734A-11
12	100.5	4.8	832	2	US-08-677-734A-12
13	96.5	4.6	834	2	US-08-677-734A-9
14	96.5	4.6	834	2	US-08-677-734A-10
15	96	4.6	473	1	US-08-597-236-13
16	96	4.6	473	1	US-08-597-236-13
17	95	4.5	888	2	US-08-956-242-13
18	95	4.5	888	2	US-08-956-242-2
19	94	4.5	626	2	US-08-956-242-2
20	94	4.5	626	2	US-09-351-215-2
21	91.5	4.4	1159	2	US-08-956-242-13
22	91.5	4.4	1159	3	US-09-351-215-13
23	91.5	4.4	1159	4	US-09-226-012-2
24	91.5	4.4	1159	4	US-09-226-012-4
25	91	4.4	606	3	US-08-620-077B-3
26	90	4.3	1872	6	US-08-620-077B-3
27	89.5	4.3	548	3	US-08-903-139B-28

28	89.5	4.3	1036	2	US-08-720-484A-5	Sequence 5, Appl
29	89.5	4.3	1036	4	US-08-953-823A-5	Sequence 5, Appl
30	89	4.3	552	3	US-09-111-752-7	Sequence 7, Appl
31	89	4.3	682	2	US-08-436-900A-4	Sequence 4, Appl
32	88	4.2	547	3	US-08-903-139B-7	Sequence 7, Appl
33	88	4.2	550	4	US-08-637-823B-3	Sequence 30, Appl
34	87.5	4.2	483	4	US-08-637-823B-4	Sequence 4, Appl
35	87	4.2	482	4	US-08-637-823B-5	Sequence 4, Appl
36	87	4.2	548	3	US-08-676-823B-5	Sequence 6, Appl
37	87	4.2	548	3	US-08-903-139B-5	Sequence 50, Appl
38	87	4.2	548	4	US-08-637-823B-2	Sequence 8, Appl
39	87	4.2	793	3	US-08-374-823B-4	Sequence 25, Appl
40	87	4.2	793	4	US-08-895-590-4	Sequence 4, Appl
41	87	4.2	1480	1	US-08-466-886-1	Sequence 17, Appl
42	87	4.2	1480	2	US-08-466-886-1	Sequence 4, Appl
43	87	4.2	1480	3	US-07-890-609-4	Sequence 4, Appl
44	87	4.2	1480	4	US-08-469-617-17	Sequence 17, Appl
45	86.5	4.1	482	4	US-08-637-823B-3	Sequence 32, Appl

## ALIGNMENTS

RESULT 1  
US-09-236-080-6  
; Sequence 6, Application US/09236080  
; Patent No. 6242217  
; GENERAL INFORMATION:  
; APPLICANT: Helen Meadows  
; APPLICANT: Conrad Chapman  
; TITLE OR INVENTION: No. 6242217el Compounds  
; FILE REFERENCE: GP30031  
; CURRENT APPLICATION NUMBER: US/09/236,080  
; CURRENT FILING DATE: 1999-01-25  
; NUMBER OF SEQ. ID NOS.: 6  
; SOFTWARE: FASTSEQ for Windows Version 3.0  
; SEQ ID NO 6  
; LENGTH: 411  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-236-080-6

Query Match	99.7%	Score 2084;	DB	Length 411;
Best Local Similarity	99.8%	Pred. No. 2.2e-211,		
Matches 410;	Conservative	0;	Mismatches 1;	Indels 0;
			Gaps 0;	
QY	1	MAAPDLDPKSAONSKPRLVSFSKPTVLASRVSDSA	KKKVTSTFLVYVLYLI	60
DB	1	MAAPDLDPKSAONSKPRLVSFSKPTVLASRVSDSA	KKKVTSTFLVYVLYLI	60
QY	61	GAATFKALDPOEISORTTIVYKOTFLAHCYNSTE	QOIYAAINAGIIPGNS	120
DB	61	GAATFKALDPOEISORTTIVYKOTFLAHCYNSTE	QOIYAAINAGIIPGNS	120
QY	121	SNQVSHMDLSSFFAGTIVITIGFGNISPRTEGKIF	IVALLGIPLEGFLLAGVDQ	180
DB	121	SNQVSHMDLSSFFAGTIVITIGFGNISPRTEGKIF	IVALLGIPLEGFLLAGVDQ	180
QY	181	LGITFGKIGIAKEVETFTKMNVSOTKIRIISTITILG	LFVALPRAVIRKHIGMSALD	240
DB	181	LGITFGKIGIAKEVETFTKMNVSOTKIRIISTITILG	LFVALPRAVIRKHIGMSALD	240
QY	241	AIIVVITLTTIGFGDVAGSDIEYLDFFKPVVEMW	AVFAVLSMIGMLRVIS	300
DB	241	AIIVVITLTTIGFGDVAGSDIEYLDFFKPVVEMW	AVFAVLSMIGMLRVIS	300
QY	301	KKTKEVGEFRAHAAEWTANTVAFKKTTRRLSVEI	DK-QIATSVKRLSAGELAGHNQ	360
DB	301	KKTKEVGEFRAHAAEWTANTVAFKKTTRRLSVEI	DK-QIATSVKRLSAGELAGHNQ	360
QY	361	ELTPCRRLTSVNHITSRREVLPPLKAESIIYNL	GLTHKATGDAVIENKK 411	
DB	361	ELTPCRRLTSVNHITSRREVLPPLKAESIIYNL	GLTHKATGDAVIENKK 411	



[illegible]

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Oy 219 CYLEFALADP---IKKHIEGSAIDAIYFVVTLTITIGDGVVA-----GGSDIE 265
Db 185 IALFVLPDPCGVHLLREL-GLSSI-SLYISVYTTTIGFGDVPPIPGANOPKEFGGMFV 242
Oy 322 TAEFEETRRLRS-----VEYDKFRQATSV-----KRLIS- 351
Db 297 TKDVGYLRRMLNELYLKVKPPYTVLDIAYTLPRNSQI-ISMRYEPAPIPSRRAESV 356
Oy 352 -AELAG-----NNHOELTPCR-----TLNVNHSF-----REYLPULK 386
Db 357 CADMGAGOREAGMWHANSOTDLTKIDREKTFETAAYH-ITDLAKVYNALATVAPPAE 416
Oy 387 AESIYLNG 394
Db 417 QEDALYLG 424

RESULT 6
US-08-332-312-4
Sequence 4, Application US/08332312
Patent No. 5559026
GENERAL INFORMATION:
APPLICANT: Price, Laura A.
APPLICANT: Pausch, Mark H.
TITLE OF INVENTION: Functional Expression of a Drosophila
TITLE OF INVENTION: Melanogaster Putative Potassium Channel in Yeast
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: US
ZIP: 07470-8426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,312
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Harrington, James J.
REGISTRATION NUMBER: P-38,711
REFERENCE/DOCKET NUMBER: 33,421
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-831-3246
TELEFAX: 201-831-3305
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-312-4

Query Match 10.5%, Score 219, DB 1, Length 336;
Best Local Similarity 26.7%, Pred. No. 7,4e-15;
Matches 60; Conservative 36; Mismatches 77; Indels 52; Gaps 6;

Oy 120 SSNOVSH-----MDLGSFFAGAVITTTIGGNTSPRI TSGKIFCIYVALGIDPLFGPL 173
Db 15 TSNEVKKNAAEETWTFPFSSSIFPAVYVTTTIGGNVPTVJNCRITWCLIFSLGIDPL---T 71
Oy 174 LAGVGDDGLGTIFGKIAKAVEDTFIK-----NNVSQT 204

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Db 72 LVNIADLAGFSLSEHVLWLVGNLTKLKLILSRKRERREHCEHSHGMDMNEEK 131  
QY 205 KIIITIIIFILGCVLPAVPAVIRHIGMSALDAIYFVITLTITGGDVGAGSDI 264  
Db 132 RI---PAFLVLAFLVYTAFGVLSMKLEPWSFSTFMTMTVGGDLMPRDGY 187  
QY 265 EYLD-----YKPVWFMIWGLAYFAVLSMIG-DMLRVY 299  
Db 188 MYIILYIIIGKFSMKKKKFKIFLGAIITTCIDLVGVYIRKI 232

## RESULT 7

US-08-749-816-4  
; Sequence 4, Application US/08749816  
; Patent No. 6013470

## GENERAL INFORMATION:

APPLICANT: Lesage, Florian  
APPLICANT: Guillemare, Eric  
APPLICANT: Fink, Michel  
APPLICANT: Duprat, Fabrice  
APPLICANT: Lazdunki, Michel  
APPLICANT: Roney, Georges  
APPLICANT: Barthelin, Jacques  
TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS,  
TITLE OF INVENTION: THEIR CLONING AND THEIR USE ESPECIALLY FOR THE SCREENING  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: WEISER & ASSOCIATES  
STREET: 230 South Fifteenth Street, Suite 500  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19102

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/749,816

FILING DATE: 15-NOV-1996  
CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:  
NAME: Weiser, Gerard J.  
REGISTRATION NUMBER: 19,763

REFERENCE/DOCKET NUMBER: 989,6351P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-875-8383  
TELEFAX: 215-875-8394

INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 383 amino acids  
TYPE: amino acid

STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-749-816-4

Query Match 8.8%; Score 184.5; DB 3; Length 383;  
Best Local Similarity 24.3%; Pred. No. 3.9e-11;  
Matches 84; Conservative 54; Mismatches 114; Indels 93; Gaps 15;

QY 11 SAQNSK-PLTSSSKPTVYASRVESDSAINWKKTKVTITFIYVVLITLGAFAKALE 69  
Db 4 SMENSKIKWLSTSKDKKATDRLSLNKLPLALHTGLVLSVYALGAYLFISIE 63  
QY 70 OPOEISORTIVYOKOTFFINQACVNSTEDELIOOIVAAINNG-----I 114  
Db 64 HPEELKREKAT-----REFODLKQOPMGNTGISIENSSEOSIEIYTKLI 108

QY 115 IPLGNSSNQ-----VSH-----WDLGSSFPFAGTV\*TI\*FGNISPTREGKIFCII 161  
Db 109 LMEEDAHNAHAEFEYFLNHIPIKDMTFSSALVFTTTV\*YGYIFPSAAGRCLIA 168  
QY 162 YALLGIPLEFGELLAGVD---QUGTIFGKIGIAVEDTFK\*---NVSOTKIRIISTII 214  
Db 169 YALLGIPLEFLVTMADIGKFAAQLVT-----HGDNNMA-----IPAAIF 208  
QY 215 ILFGCVLPAVPAV---IFPHIGMSALDAIYFVITLTI\*EGCDVYAGSDIEYIDFYK 271  
Db 209 V---CLLF-AVPLVGPILCTSNITLYLDSVPSLSIFILGFDLTPDMNVITHVLF-- 262  
QY 272 PVVWFMIWGLAYFAVLSMIG---DMLRVISK---K\*VGE 309  
Db 263 -----LAVGVILVITTLTDIVAEMIDRVHYMGRHNGKA\*LAGK 301

## RESULT 8

US-08-749-816-3  
; Sequence 3, Application US/08749816  
; Patent No. 6013470

## GENERAL INFORMATION:

APPLICANT: Lesage, Florian  
APPLICANT: Guillemare, Eric  
APPLICANT: Fink, Michel  
APPLICANT: Duprat, Fabrice  
APPLICANT: Lazdunki, Michel  
APPLICANT: Roney, Georges  
APPLICANT: Barthelin, Jacques  
TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS,  
TITLE OF INVENTION: THEIR CLONING AND THEIR USE ESPECIALLY FOR THE SCREENING  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: WEISER & ASSOCIATES  
STREET: 230 South Fifteenth Street, Suite 500  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19102

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/749,816

FILING DATE: 15-NOV-1996  
CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:  
NAME: Weiser, Gerard J.  
REGISTRATION NUMBER: 19,763

REFERENCE/DOCKET NUMBER: 989,6351P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-875-8383  
TELEFAX: 215-875-8394

INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 347 amino acids  
TYPE: amino acid

STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-749-816-3

Query Match 7.7%; Score 160.5; DB 3; Length 347;  
Best Local Similarity 23.7%; Pred. No. 1.1e-08;  
Matches 57; Conservative 53; Mismatches 88; Indels 43; Gaps 10;

QY 52 LVVYVLIIGAVFKALPOEISORTIVYOKOTIAC\*HACVNSTEDELIOOIVAAIN 111  
Db 44 IITLVENLIGAGIFYLAE-----TONSSSELNENSEVSK--CLHNPDIG--GKITAEMK 93





OY 316 EWTANVTAEFKET 328  
Db 335 RYTMKMLASCAET 347

## RESULT 13

US-08-677-734A-9  
; Sequence 9, Application US/08677734A  
; Patent No. 5871919  
; GENERAL INFORMATION:  
; APPLICANT: Brant, Steven R.  
; APPLICANT: Yun, Chris C.H.  
; APPLICANT: Donowitz, Mark  
; APPLICANT: Tse, Chung-Ming  
; TITLE OF INVENTION: Cloning, Tissue Distribution, and  
; TITLE OF INVENTION: Functional Analysis of the Human Na<sup>+</sup>/H<sup>+</sup> Exchanger Isoform,  
; TITLE OF INVENTION: NHE3.  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
; ADDRESS: Dunnet  
; STREET: 1300 I Street, N.W., Suite 700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/677,734A  
; FILING DATE: 10-JUL-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fordis, Jean B.  
; REGISTRATION NUMBER: 32,984  
; REFERENCE/DOCKET NUMBER: 05387, 0043-00000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 408-4000  
; TELEFAX: (202) 408-4400  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 834 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-677-734A-9

Query Match 4.6%; Score 96.5; DB 2; Length 834;

Best Local Similarity 20.4%; Pred. No. 0.24; Mismatches 94; Indels 119; Gaps 15;

OY 52 LVVAVYLIIIGAFAKALEQPEISORTTIVIQKOTFLAQHACVSTELDELIOQIVAIN 111  
Db 87 LLIYGLVGLGIWMA-----DHIASFLTPVFFVYLLPPIV--LD 126  
OY 112 AGIPLGNSSNOVSHMDGSSFFPA--GTVITTTIGFNGISPRTEGKIFCIITVALLGIP 169  
Db 127 AGYF---MPRLFEFGNGITLLVAAGTVWNA-----ATTGISTL 162  
OY 170 FGLIAG-VGD-QUG---TTFGKIAKVEDTFLKMNVSQTKIRISITIFILG-CVLF 222  
Db 163 YGVLISGLMGLOQLGLDFLFGSLMAADPVAVL--AFEEVHVNEVLFTIVGESL 220  
OY 223 VALPAVIFKHIEGMSALDAIVFVITTTITIGFGYVAGSGSIEVLFKPKVPMFMI----- 278  
Db 221 DAVIVLVINFESEVAL-----GGDNVTVGDVCKVIGVSEFVSLG 260

OY 279 --LVGLAYFAVLNIGDM---LRVI----- 299  
Db 261 GTLVGVV-FAFLLSLVTRFTKRVRIEFGFVITSLYSY--SEMLSALDAITFCGICC 319  
OY 300 SKTKKEEYGEFRAHAEBWTANVTAEFKET 328  
Db 320 QKYVKNISQOSATVRYTMKMLASCAET 348

## RESULT 14

US-08-677-734A-10  
; Sequence 10, Application US/08677734A  
; Patent No. 5871919  
; GENERAL INFORMATION:  
; APPLICANT: Brant, Steven R.  
; APPLICANT: Yun, Chris C.H.  
; APPLICANT: Donowitz, Mark  
; APPLICANT: Tse, Chung-Ming  
; TITLE OF INVENTION: Cloning, Tissue Distribution, and  
; TITLE OF INVENTION: Functional Analysis of the Human Na<sup>+</sup>/H<sup>+</sup> Exchanger Isoform,  
; TITLE OF INVENTION: NHE3.  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
; ADDRESS: Dunnet  
; STREET: 1300 I Street, N.W., Suite 700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/677,734A  
; FILING DATE: 10-JUL-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fordis, Jean B.  
; REGISTRATION NUMBER: 32,984  
; REFERENCE/DOCKET NUMBER: 05387, 0043-0000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 408-4000  
; TELEFAX: (202) 408-4400  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 834 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-677-734A-10

Query Match 4.6%; Score 96.5; DB 2; Length 834;

Best Local Similarity 20.4%; Pred. No. 0.24; Mismatches 94; Indels 119; Gaps 15;

OY 52 LVVAVYLIIIGAFAKALEQPEISORTTIVIQKOTFLAQHACVSTELDELIOQIVAIN 111  
Db 87 LLIYGLVGLGIWMA-----DHIASFLTPVFFVYLLPPIV--LD 126  
OY 112 AGIPLGNSSNOVSHMDGSSFFPA--GTVITTTIGFNGISPRTEGKIFCIITVALLGIP 169  
Db 127 AGYF---MPRLFEFGNGITLLVAAGTVWNA-----ATTGISTL 162  
OY 170 FGLIAG-VGD-QUG---TTFGKIAKVEDTFLKMNVSQTKIRISITIFILG-CVLF 222  
Db 163 YGVLISGLMGLOQLGLDFLFGSLMAADPVAVL--AFEEVHVNEVLFTIVGESL 220  
OY 223 VALPAVIFKHIEGMSALDAIVFVITTTITIGFGYVAGSGSIEVLFKPKVPMFMI----- 278

Search completed: August 28, 2001, 17:06:22  
Job time: 526 sec

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Db 221 DATVVLVYNVEESFVAL-----GDNVTVGDCVKIVSFFVSLG 260
QY 279 --LVGLAYFAAVLSMIGD--LRVI-----299
Db 261 GTIVGVV-FAPLLSLVTRFKHVRRIIEPGFVLIISYLSITSEMLSALAILTFGICCC 319
QY 300 SKRTKEEVEGFRAHAAEMWTANVTAEKET 328
Db 320 OKYVKANISEOSATYVRYTMKMLASSAET 348
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## RESULT 15

```
US-08-597-236-13
; Sequence 13, Application US/08597236
; Patent No. 5733765
; GENERAL INFORMATION:
; APPLICANT: STINGELE, Francesca
; APPLICANT: MOLLET, Beat
; TITLE OF INVENTION: LACTIC BACTERIA PRODUCING
; TITLE OF INVENTION: EXOPOLYSACCHARIDES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americans
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/597,236
; FILING DATE:
; CLASSIFICATION: 426
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95201669,9
; FILING DATE: 20-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Fanucci A., Allan
; REGISTRATION NUMBER: 30256
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 473 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-597-236-13
```

Query Match 4.6%; Score 96; DB 1; Length 473;

Best local Similarity 22.8%; Pred. No. 0.12;

Matches 47; Conservative 33; Mismatches 52; Indels 74; Gaps 10;

```
QY 43 KMKTVSTIFLVVLYLLIGAAYFAKLEQPEISORTIIVOKOTFLAQHACVNSTEDEL 102
Db 280 KSYVYSDFEYHLYATFLGLGSAFMIVAKP-----I 309
QY 103 IQQIVAAINAGIPLGSSNOVSHMD-----IGSSF--FFAGTVITTIGGNISPR 151
Db 310 VERVV-----SSDYASSQVYVPRFMSMLFSSFSDFGNTYIA-----AKQ 350
QY 152 TEG-----GKFCITVALLGIPLEGFLLAGVDLG--TIRGKIAYVEDTFIKWNS 202
Db 351 TKGVFMTSYIGTVLCVLLQVYLLPIIGLDAGLSAMLGFLTF--LLRVKDT-QKFFVI 406
QY 203 QTKIRI-ISTIFILFCGVFLVALPA 227
Db 407 QIKWRIFISMILIVLAQHILCLFLPLPS 432
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Db 206 SKRELKQSDHEHLREIAEVSPLYDLVLAGLFVFAIGSAVPIWMNOLTYFDSVYFS 265  
 QY 246 VITLTTIGFDYVAGSDIEYLDPFYKPVWFWILVGLAYFAAVLSMIGDMLRV 299  
 Db 266 YMSLTITGLADIYP-----RRMDFLPTL-IYITIGLMTLTALEQADLVFRIV 313

## RESULT 14

T30037

hypothetical protein F20A1.7 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999

C:Accession: T30037

R:Galtung, S.; Wu, X.

A:Submitted to the EMBL Data Library, March 1996

A:Description: The sequence of C. elegans cosmid F20A1.

A:Reference number: Z20726

A:Accession: T30037

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-1539 &lt;GAT&gt;

A:Cross-references: EMBL:U053150; PIDN:AAA96127.1; GSPDB:GN00023; CESP:F20A1.7

A:Experimental source: strain Bristol N2; clone F20A1

C:Genetics:

A:Gene: CESP:F20A1.7

A:Map position: 5

A:Introns: 19/3; 41/2; 71/2; 110/3; 135/2; 190/1; 246/1; 287/3; 491/3; 598/2; 983/2; 110

Query Match 12.1%; Score 252.5; DB 2; Length 1539;

Best Local Similarity 22.3%; Pred. No. 3.6e-12;

Matches 96; Conservative 72; Mismatches 131; Indels 131; Gaps 16;

QY 25 KPNVLA SRVSDSAIN--VMKN-----KTVSTFLVNV--LYLIGAAVEFALE 69  
 Db 52 KPSVLAASIR-ESNISKRRKLTYSCTPPIKKLTSTFKLLITIGLSTGAIHEWYLE 110  
 QY 70 QPQISQRTTIVIOKQFFIAQHACVNSTELDELIOQIVAAINAGIIPLGSSNOVSHW-- 127  
 Db 111 VPIVLDLAREGDFHQRK-----IAREVMVNLRAIYDNRREDREERMKH 153  
 QY 128 -----DLG-----SSPFAQTVITTTIGFNI SPRTGCKITFCIIYALLGI 167  
 Db 154 AILKFEDIDLEPVEIETVWTFFMSSFLYAGTIFTTIGYGNACKTRAGQATATVYAFVGI 213  
 QY 168 PLF-----GFLA-----GYGQ-----LGIIRGKI-----AKVEDTFI 197  
 Db 214 PIMLVMLTSLNPLKWKIKITNGVSDMTLYIGVRLGITVIRODEVOKRLRYTKLAKTMK 273  
 QY 198 KMNVSQ-----TKRIIST-----IIFILFGVLFVALPAVIE 230  
 Db 274 RMLLSKRGASSTAIASNSENRNSTPEDDEEEIHODPVLTSLATVAMITLSAAVF 333  
 QY 231 KHIKGSALDAITFYVITLTTIGFGDYVAGSDIEYLDPFYKPVWFWILVGLAYFAAVLS 290  
 Db 334 CLEEDMTFTSFYFCISLTITIGLGVTPANPE-----YMIATFGVIVIGLSMLTVCID 387  
 QY 291 MIGD-----MLRYSKTKTEVEGFEFRHAHAEMTANVTAEFKTRRRRL-----SVEIY 337  
 Db 388 VLDKLAQMTMALOKLLITLMEAVKSGDPNAASAMMAGFGGRAKFLMPLISKNEGAKVM 447  
 QY 338 DKFORATSVK 347  
 Db 448 DKFKODOSKK 457

## RESULT 15

T26229

hypothetical protein W06D12.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999

C:Accession: T26229

R:Baslam, V.

submitted to the EMBL Data Library, November 1996  
 A:Reference number: Z20177

A:Accession: T26229

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-444 &lt;MIL&gt;

A:Cross-references: EMBL:282073; PIDN:CAB04923.1; N:DB:GN00023; CESP:W06D12.2

A:Experimental source: clone W06D12

C:Genetics:

A:Gene: CESP:W06D12.2

A:Map position: 5

A:Introns: 70/3; 127/1; 170/1; 197/3; 326/1; 405/1

Query Match 11.8%; Score 247; DB 2; Length 444;

Best Local Similarity 20.3%; Pred. No. 2.3e-11;

Matches 79; Conservative 76; Mismatches 79; Indels 108; Gaps 11;

QY 53 VVVLYLITGAVF-----KALEQPOEISQRTTIVLCSTF-----AOHACV 94  
 Db 23 VLIYVSFLGGLVLCFAENEKSLKHDNMRVLRISIAKCFVQRLQNNYSGNGSSSEF 82  
 QY 95 NSTELDELIOQIVAAINAGIIPLGSSNOVSHWDLSSFFACTVITTTIGFNI SPRTG 154  
 Db 83 SETRLRRVISEYDAAMGIST-----DSKMTKTRMDINGGLVNGTIYTTIGYGLAAETIW 137  
 QY 155 GKICFIYALLGIPRLGFLLAGYGDQDGTI---FGKIAKVIJTFIKMNSQTKIR---- 207  
 Db 138 GRICTMLYAMIGIPIVINIINDGNMLFVDFHWONIGKQIIOSLRQKRRKVSLEE 197  
 QY 208 -----IISTIIFFTCVLFVALPAVIFKHIEGW 236  
 Db 198 GSDIKTPIMETSTPPSPQNPNGTRPIPLLVILVLFGLKIVAV-----FAYFENW 250  
 QY 237 SALDAITFYVITLTTIGFGDY-----VAGSDIEYLDPFYKPVWFWILVGLAYFAAVLSM 291  
 Db 251 TLFEVSFFPISMTTIGFGDFTPSHTVAVGGIV-----FILGLSVSMCINV 298  
 QY 292 IGDMLRYSKTKTEV-GEFRHAHAEMTANVTAE-----FKETRRRLS 333  
 Db 299 IOMOLETIFNOIVORLNDKKN-----TLSVAAESKRLV--VSEFGSIDPSKKTKTRD 353  
 QY 334 VEIYDKFORATSVKRLSALAGNHOEL 362  
 Db 354 GNVAKESNMENGNKLLMRFMSNHQKKM 382

Search completed: August 28, 2001, 17:07:05  
 Job time: 474 sec





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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 28, 2001, 17:13:13 : Search time 21.03 Seconds  
(without alignments)  
669.472 Million cell updates/sec

Title: US-09-503-089a-4  
Perfect score: 2090  
Sequence: 1 MAAPDLDPKSAQNSKPKRL.....LNGLPHCGEDIAVIENMK 411

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues  
Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: SwissProt\_39.\*  
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2090	100.0	411	CIW2_MOUSE	P97438 mus musculu
2	2011	96.2	426	CIW2_HUMAN	O95069 homo sapien
3	797	38.1	393	CIW4_HUMAN	O9ny88 homo sapien
4	770.5	36.9	398	CIW4_MOUSE	O88454 mus musculu
5	420	20.1	499	CIW5_HUMAN	O95279 homo sapien
6	376.5	18.0	336	CIW1_HUMAN	O00160 homo sapien
7	370	17.7	336	CIW1_MOUSE	O08561 mus musculu
8	370	17.7	394	CIW3_HUMAN	O14649 homo sapien
9	351	16.8	409	CIW3_MOUSE	O35111 mus musculu
10	342	16.4	411	CIW6_HUMAN	O54912 rattus norv
11	342	16.4	313	CIW6_MOUSE	O9y257 homo sapien
12	325	15.6	1001	ORX1_DROME	O94526 drosophila
13	305.5	14.6	307	CIW7_MOUSE	O9y251 mus musculu
14	300.5	14.4	307	CIW7_HUMAN	O9y252 homo sapien
15	217	10.4	691	TKR1_YEAST	P40310 saccharomyc
16	215.5	10.3	335	TKR8_CAEEL	P44010 caenorhabdi
17	122	5.8	238	YWS1_CAEEL	O10937 caenorhabdi
18	121	5.8	604	CI01_MOUSE	P97414 mus musculu
19	119	5.7	676	CI01_HUMAN	P51787 homo sapien
20	107.5	5.1	461	YIFR_SALTY	P37456 salmonella
21	106.5	5.1	334	PIT_RHME	O30459 rhizobium m
22	105	5.0	872	ATCL_MYCPN	P78036 mycoplasma
23	103.5	5.0	649	OOX1_BACSU	P34956 bacillus su
24	102.5	4.9	839	NAH3_DIMA	O28362 didelphis m
25	102	4.9	451	YVS3_RHME	P33653 rhizobium m
26	101.5	4.9	831	NAH3_RAT	P26433 rattus norv
27	101	4.8	412	O85D_DROME	O9vhs2 drosophila
28	100.5	4.8	342	COBD_SYNX3	P74475 synecocyst
29	100.5	4.8	832	SSRS_MOUSE	O08858 mus musculu
30	100.5	4.8	362	NAH3_RABIT	P26442 oryctolagus
31	100	4.8	337	COX1_RHEAM	O03546 thea americ
32	100	4.8	402	Y718_METJA	O58138 methanococc
33	100	4.8	533	MYIN_SYNY3	O55179 synecocyst

34	99	4.7	395	1	CDSA_MYCPN	P75160 m putative
35	98.5	4.7	520	1	TDT_BOVIN	P06526 bos taurus
36	98.5	4.7	601	1	CIK5_MUSPF	P79197 musceta put
37	98	4.7	305	1	CDSA_MYGE	O49433 m putative
38	98	4.7	333	1	Y13B_METJA	O57604 methanococc
39	98	4.7	635	1	CI04_HUMAN	P56696 homo sapien
40	97.5	4.7	400	1	TYRP_HAEIN	P44727 haemophilus
41	97.5	4.7	602	1	CIK5_MOUSE	O61762 mus musculu
42	97	4.6	275	1	TAUC_ECOLI	O47539 escherichia
43	97	4.6	579	1	YH83_SCHPO	O9P502 schizosacch
44	97	4.6	602	1	CIK5_RAT	P19024 rattus norv
45	96.5	4.6	663	1	CNG2_BOVIN	O03041 bos taurus

ALIGNMENTS

RESULT 1  
ID CIW2\_MOUSE STANDARD; PRT; 411 AA  
AC P97438;  
DT 01-OCT-2000 (Rel. 40, Created)  
DT 01-OCT-2000 (Rel. 40, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE POTASSIUM CHANNEL SUBFAMILY K MEMBER 2 (OUTW) RECTIFYING POTASSIUM  
DE CHANNEL PROTEIN TREK-1 (TWO-PORE POTASSIUM CHANNEL TPCK1) (TREK-1 K+  
DE CHANNEL SUBUNIT).  
GN KCNK2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.  
OX NCBI\_Taxid=10090;  
RN [1]  
RP SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.  
RC TISSUE-Brain;  
RX MEDLINE=97157476; PubMed=9003761;  
RA Fink M., Duprat F., Lesage F., Reyes R., Romey J., Heurteaux C.,  
RA Lazdunski M.;  
RT cloning, functional expression and brain localization of a novel  
RT unconventional outward rectifier K+ channel.  
RL EMO J. 15:6854-6862(1996).  
RN [2]  
RP REVISIONS.  
RC TISSUE-Brain;  
RA Fink M., Duprat F., Lesage F., Reyes R., Romey J., Heurteaux C.,  
RA Lazdunski M.;  
RT Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP MEDLINE=99254548; PubMed=10321245;  
RA Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.;  
RT Inhalational anesthetics activate two-pore K+ main background K+  
RT channels.";  
RL Nat. Neurosci. 2:422-426(1999).  
CC - FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL.  
CC - SUBUNIT: HOMODIMER (POTENTIAL).  
CC - SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).  
CC - TISSUE SPECIFICITY: HIGH EXPRESSION IN BRAIN AND LUNG. ALSO  
CC DETECTED IN KIDNEY, HEART AND SKELETAL MUSCLE. NOT DETECTED IN  
CC LIVER. IN THE BRAIN, HIGHEST EXPRESSION IN OLFACTORY BULB,  
CC HIPPOCAMPUS AND CEREBELLUM.  
CC - MISCELLANEOUS: INHIBITED BY BARIUM. ACTIVATED BY VOLATILE GENERAL  
CC ANESTHETICS SUCH AS CHLOROFORM, DIETHYL ETHER, HALOTHANE AND  
CC ISOFLURANE.  
CC - SIMILARITY: BELONGS TO THE TWO PORE DOM. FAMILY OF POTASSIUM  
CC CHANNELS.  
CC -----  
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or send an email to [license@sb-slb.ch](mailto:license@sb-slb.ch).

CC EMBL: U73488; AAC53005.2; -  
 CC MGD: MG1:109366; Kcnk2.  
 DR InterPro: IPR000099; -  
 DR InterPro: IPR001622; -  
 DR InterPro: IPR003280; -  
 DR Pfam: PF02034; TWIK\_channel; 1.  
 DR PRINTS: PRO1333; 2PORECHANNEL.  
 KW Ionic channel; Transmembrane; Ion transport; Potassium transport;  
 Glycoprotein.

FT DOMAIN 1 46 CYTOPLASMIC (POTENTIAL).  
 FT TRANSSEM 47 67 POTENTIAL.  
 FT DOMAIN 129 155 PORE-FORMING (POTENTIAL).  
 FT TRANSSEM 157 177 POTENTIAL.  
 FT DOMAIN 178 207 CYTOPLASMIC (POTENTIAL).  
 FT TRANSSEM 208 228 POTENTIAL.  
 FT DOMAIN 238 268 PORE-FORMING (POTENTIAL).  
 FT TRANSSEM 273 293 POTENTIAL.  
 FT DOMAIN 294 411 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 378 411 ESSENTIAL FOR CHLOROFORM AND HALOTHANE SENSITIVITY.

FT DOMAIN 354 411 REQUIRED FOR BASAL CHANNEL ACTIVITY.  
 FT CARBOHYD 95 95 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 411 AA; 45297 MW; 8f976DDD103EFA05 CRC64;

Query Match 100.0%; Score 2090; DB 1; Length 411;  
 Best Local Similarity 100.0%; Pred. No. 6,4e-136;  
 Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPDLDPKSAQNSKPRLSFSSKPTVLASRYESDSAINVMKMKVSTFLVVLII 60  
 DB 1 MAAPDLDPKSAQNSKPRLSFSSKPTVLASRYESDSAINVMKMKVSTFLVVLII 60  
 QY 61 GAAVFALEPOEISORTTIVIOKQFIAOHACVNSTEDELIIQIYVAIINAGIIPLGNS 120  
 DB 61 GAAVFALEPOEISORTTIVIOKQFIAOHACVNSTEDELIIQIYVAIINAGIIPLGNS 120  
 QY 121 SNOVSHMDLGSFFPAGTIVTTIGFNGISPRTEGKIFCTIYALGLPLGELLAGVDQ 180  
 DB 121 SNOVSHMDLGSFFPAGTIVTTIGFNGISPRTEGKIFCTIYALGLPLGELLAGVDQ 180  
 QY 181 LGTIFGKIAKVEDTFIKMNSQTKIRIISTIIIFLEGCVLPAVPAVIRKHNIEGMSALD 240  
 DB 181 LGTIFGKIAKVEDTFIKMNSQTKIRIISTIIIFLEGCVLPAVPAVIRKHNIEGMSALD 240  
 QY 241 AIFPVVITLTITIGFGDYVAGSDIEYLDYFKKPYVWEIILVGLAVFAVLSMIGDWLRVIS 300  
 DB 241 AIFPVVITLTITIGFGDYVAGSDIEYLDYFKKPYVWEIILVGLAVFAVLSMIGDWLRVIS 300  
 QY 301 KTKKEVEGEFRAHAAEVTAETAEKTRRLSVEIYDKORATSVKRSKASAEIAGHNQ 360  
 DB 301 KTKKEVEGEFRAHAAEVTAETAEKTRRLSVEIYDKORATSVKRSKASAEIAGHNQ 360  
 QY 361 ELTPCRRTLSVNHLSREVLPLPLKAESIYINGLTPHCAGEDIAVEIENK 411  
 DB 361 ELTPCRRTLSVNHLSREVLPLPLKAESIYINGLTPHCAGEDIAVEIENK 411

RESULT 2  
 ID C1W2\_HUMAN STANDARD; PRT; 426 AA.  
 AC 095069; O9UNE3;  
 DT 01-OCT-2000 (Rel. 40, Created)  
 DT 01-OCT-2000 (Rel. 40, Last sequence update)  
 DE POTASSIUM CHANNEL, SUBFAMILY K MEMBER 2 (OUTWARD RECTIFYING POTASSIUM CHANNEL, PROTEIN TREK-1) (TWO-PORE POTASSIUM CHANNEL TRPC1) (TREK-1 K+ CHANNEL, SUBUNIT).  
 GN KCNK2 OR TREK.  
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9254548; PubMed=1021245;  
 RA Patel A.J., Honore E., Lesage F., Fink M., Romo G., Lazdunski M.;  
 RT "Inhalational anesthetics activate two-pore-domain background K+ channels.";  
 RL Nat. Neurosci. 2:422-426(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA Price L.A., Hellings S.E., Hayashi J.H., Paul J.H., M.H.;  
 RL Submitted (MAY-1997) to the EMBL/Genbank/DBJ databases.  
 CC -1- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL.  
 CC -1- SUBUNIT: HOMODIMER (POTENTIAL).  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).  
 CC -1- MISCELLANEOUS: ACTIVATED BY VOLATILE GASES AND ANESTHETICS SUCH AS CHLOROFORM, HALOTHANE AND ISOFLURANE.  
 CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM CHANNELS.  
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CC EMBL: AF129399; AAD47569.1; -  
 CC EMBL: AF004711; AAD01203.1; -  
 CC MIM: 603219; -  
 DR DR InterPro: IPR000099; -  
 DR DR InterPro: IPR001622; -  
 DR DR InterPro: IPR003280; -  
 DR DR Pfam: PF02034; TWIK\_channel; 1.  
 DR DR PRINTS: PRO1333; 2PORECHANNEL.  
 KW Ionic channel; Transmembrane; Ion transport; Potassium transport;  
 Glycoprotein.

KW DOMAIN 1 61 CYTOPLASMIC (POTENTIAL).  
 FT TRANSSEM 62 82 POTENTIAL.  
 FT DOMAIN 144 170 PORE-FORMING (POTENTIAL).  
 FT TRANSSEM 172 192 POTENTIAL.  
 FT DOMAIN 193 223 CYTOPLASMIC (POTENTIAL).  
 FT TRANSSEM 224 244 POTENTIAL.  
 FT DOMAIN 253 283 PORE-FORMING (POTENTIAL).  
 FT TRANSSEM 288 308 POTENTIAL.  
 FT DOMAIN 309 426 ESSENTIAL FOR CHLOROFORM AND HALOTHANE SENSITIVITY (BUT NOT POTENTIAL).  
 FT DOMAIN 378 426 REQUIRED FOR BASAL CHANNEL ACTIVITY (BY SIMILARITY).  
 FT DOMAIN 354 426 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 134 134 MISSING (IN REF. 2).  
 FT CONFLICT 2 16 RLV -> DWL (IN REF. 2).  
 FT CONFLICT 309 311 S -> N (IN REF. 2).  
 FT CONFLICT 391 391 S -> T (IN REF. 2).  
 FT CONFLICT 411 411 A -> T (IN REF. 2).  
 SQ SEQUENCE 426 AA; 47016 MW; 2ABA23356D400; CRC64;

Query Match 96.2%; Score 2011; DB 1; Length 426;  
 Best Local Similarity 95.1%; Pred. No. 1.7e-14;  
 Matches 391; Conservative 13; Mismatches 7; Indels 0; Gaps 0;

QY 1 MAAPDLDPKSAQNSKPRLSFSSKPTVLASRYESDSAINVMKMKVSTFLVVLII 60  
 DB 16 VAAFDLDPKSAQNSKPRLSFSTKPTVLASRYESDTTIVKMKVSTFLVVLII 75  
 QY 61 GAAVFALEPOEISORTTIVIOKQFIAOHACVNSTEDELIIQIYVAIINAGIIPLGNS 120  
 DB 11 GAAVFALEPOEISORTTIVIOKQFIAOHACVNSTEDELIIQIYVAIINAGIIPLGNS 120

```

Db 76 GATYFAKLEDPHEISQRTTYIKQOTFISQHSVCNSTELDELIOIVAAINAGIIPLGNT 135
QY 121 SMOVSHMDLSSFFPAGTAVITTTIGFNGINSPRTGKIFCIITIALGIPLEFLLAGVGDQ 180
Db 136 SNOASHMDLSSFFPAGTAVITTTIGFNGINSPRTGKIFCIITIALGIPLEFLLAGVGDQ 195
QY 181 LGTIFGKGIKAVETFTFKMNSQTKIRIISTITIFLFGCVLFAVLPVAVIEKHIGMSALD 240
Db 196 LGTIFGKGIKAVETFTFKMNSQTKIRIISTITIFLFGCVLFAVLPVAVIEKHIGMSALD 255
QY 241 AIYVVVITLTTIGFDVAGGSDEIYDFYKPVVFWMLVGLAFPAVLISGMLVAVIS 300
Db 256 AIYVVVITLTTIGFDVAGGSDEIYDFYKPVVFWMLVGLAFPAVLISGMLVAVIS 315
QY 301 KTKEEVGEFRAHAEMTANTVAFETRRRLSVEIDKFORATSVKRLSAELAGNHQ 360
Db 316 KTKEEVGEFRAHAEMTANTVAFETRRRLSVEIDKFORATSVKRLSAELAGNHQ 375
QY 361 ELTPCRRTLSVNLTSREVLPLLKAESIYLNGLTFPHCGEDIAVIENMK 411
Db 376 ELTPCRRTLSVNLTSREVLPLLKAESIYLNGLTFPHCGEDIAVIENMK 426

RESULT 3
C1M4_HUMAN STANDARD; PRT; 393 AA.
AC GNNGS8;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DE POTASSIUM CHANNEL SUBFAMILY K MEMBER 4 (TWIK-RELATED ARACHIDONIC ACID-
  STIMULATED POTASSIUM CHANNEL PROTEIN) (TRAAK).
GN KCNK4 OR TRAAK.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Brain;
RX PubMed-11042359;
RA Chapman C.G., Meadows H.J., Godden R.J., Campbell D.A., Duckworth M.,
  Keisell R.E., Nurdock P.R., Randall A.D., Rennie G.I., Glover I.S.;
  "Cloning, localisation and functional expression of a novel human,
  RT cerebellum specific, two pore domain potassium channel.";
  Brain Res. Mol. Brain Res. 82:74-83(2000).
RL [2]
RN SEQUENCE FROM N.A.
RC TISSUE-Frontal cortex;
RA Gray A.T.;
RT "Assignment of KCNK4 encoding the human potassium channel TRAAK to
  RT chromosome 11.";
  Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: VOLTAGE INSENSITIVE, INSTANTANEOUS, OUTWARDLY RECTIFYING
  CC POTASSIUM CHANNEL. OUTWARD RECTIFICATION IS REVERSED AT HIGH
  CC EXTERNAL K+ CONCENTRATIONS (BY SIMILARITY).
  CC -1- SUBUNIT: HOMODIMER (POTENTIAL).
  CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
  CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
  CC CHANNELS.
  CC -----
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  CC use by non-profit institutions as long as its content is in no way
  CC modified and this statement is not removed. Usage by and for commercial
  CC entities requires a license agreement (See http://www.isb.ch/announce/
  CC or send an email to license@isb-sib.ch).
  CC -----
  CC EMBL: AF248242; AAC31731.1;
  CC EMBL: AF247042; AAF64062.1; ALT_INIT.
  CC DR InterPro: IPR001622;
  CC DR InterPro: IPR003280;

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DR PRINTS: PR01333; 2PORECHANNEL.
KW Ionic channel; Transmembrane; Ion transport; Potassium transport;
  KW Glycoprotein.
FT DOMAIN 1 3
FT TRANSMEM 4 24
FT TRANSMEM 89 113
FT TRANSMEM 118 138
FT TRANSMEM 140 171
FT TRANSMEM 172 192
FT TRANSMEM 197 221
FT TRANSMEM 234 254
FT TRANSMEM 255 393
FT CARBOHYD 78 78
FT CARBOHYD 82 82
FT CONFLICT 328 328
FT CONFLICT 328 328
SQ SEQUENCE 393 AA; 42704 MW; 7E1B53A0A9AL57D CRC64;

Query Match 38.1%; Score 797; DB 1; Length 393;
Best Local Similarity 51.1%; Pred. No. 1.2e-4;
Matches 145; Conservative 60; Mismatches 27; Indels 2; Gaps 1;

QY 42 MKKTVSTIFLVVLYLITIGANVFAKLEDPQESQRTTYIKQOTFIAQACVNSTELDE 101
Db 1 MRSTTLALALVLYLVSGALYFRALEOPHEQAOQREL...PEKFLRAHCPVSDDELGL 60
QY 102 LIOOIVAINAGIIPLGNSNOVSH--WDGSSFFPAGTV...IGFNGINSPRTGKIFC 159
Db 61 LIKEVADALGGADPEPNSNSNSHSAWDGSAFFSGTTLTGCVNVALRTDAGRFLC 120
QY 160 IYVALGIPLEFLLAGVGDQITFEKGIKAVEDFTIK...SOTKRIISTITIFLFGC 219
Db 121 IFVALVGIPELGIILAGVGRGLSSLRHGIGHIEAIFLN...VELRVLSAMFLILIGC 180
QY 220 VLFVALVAFKFKIEGSSALDAITFVYITLTTIGFDVAGGSDEIYDFYKPVVFWML 279
Db 181 LFLVLPFTFVFCVMEDESKAEIYFVITLTVGFDVAGADRDOSPAPVPLVFWML 240
QY 280 VGLAFPAVLISMIGDMLRVISKTKKEEVEFRAHAEMTANTV 323
Db 241 LGLAFFASVLTITIGNMLRVVSRRTRAEMGILTAQAASTGIVTA 284

RESULT 4
C1M4_MOUSE STANDARD; PRT; 398 AA.
AC 088454;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE POTASSIUM CHANNEL SUBFAMILY K MEMBER 4 (TWIK-RELATED ARACHIDONIC ACID-
  STIMULATED POTASSIUM CHANNEL PROTEIN) (TRAAK).
GN KCNK4 OR TRAAK.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Brain;
RX MBDLINE-98292450; PubMed-9628867;
RA Fink M., Lesage F., Duprat F., Heurteaux C., Reyes R., Fosset M.,
  Lazdunski M.;
  "A neuronal two p domain K+ channel stimulus 1 by arachidonic acid and
  RT polyunsaturated fatty acids.";
  EMBO J. 17:3297-3308(1998).
  CC [2]
  CC ACTIVATION.
  CC MBDLINE-99254548; PubMed-10321245;
  CC RA Patel A.J., Honore E., Lesage F., Fink M., May G., Lazdunski M.;
  CC "Inhalational anesthetics activate two pore-domain background K+
  CC channels.";
  CC Nat. Neurosci. 2:422-426(1999).
  CC RL

```

CC -1- FUNCTION: VOLTAGE INSENSITIVE, INSTANTANEOUS, OUTWARDLY RECTIFYING  
 CC POTASSIUM CHANNEL. OUTWARD RECTIFICATION IS REVERSED AT HIGH  
 CC EXTERNAL K+ CONCENTRATIONS.  
 CC -1- SUBUNIT: HOMODIMER (POTENTIAL).  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND  
 CC 2/TRAAT/TRANCATD; ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, SPINAL CORD AND EYE. NOT  
 CC DETECTED IN HEART, SKELETAL MUSCLE, LIVER, LUNGS, KIDNEY AND  
 CC TESTIS.  
 CC -1- MISCELLANEOUS: ACTIVATED BY ARCHIDONIC ACID AND OTHER UNSATURATED  
 CC FATTY ACIDS. NOT AFFECTED BY VOLATILE GENERAL ANAESTHETICS SUCH AS  
 CC CHLOROFORM, DIETHYL ETHER, HALOTHANE AND ISOFLOURANE.  
 CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM  
 CC CHANNELS.  
 CC -----  
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 CC -----  
 CC EMBL: AF056492; AAC40181.1; -.  
 CC DR MGD; MGI:1298234; Kcnk4.  
 CC DR InterPro: IPR000099; -.  
 CC DR InterPro: IPR001622; -.  
 CC DR InterPro: IPR003280; -.  
 CC DR Pfam: PR02034; TWIK\_Channel; 1.  
 CC DR PRINTS; PRO1333; 2PORECHANNEL.  
 CC KW Ionic channel; Transmembrane; Ion transport; Potassium transport;  
 CC Glycoprotein; Alternative splicing.  
 CC FT DOMAIN 1 3  
 CC FT TRANSMEM 4 24 CYTOPLASMIC (POTENTIAL).  
 CC FT DOMAIN 89 113 PORE-FORMING (POTENTIAL).  
 CC FT TRANSMEM 119 139 POTENTIAL.  
 CC FT DOMAIN 140 171 CYTOPLASMIC (POTENTIAL).  
 CC FT TRANSMEM 172 192 POTENTIAL.  
 CC FT DOMAIN 198 222 PORE-FORMING (POTENTIAL).  
 CC FT TRANSMEM 235 255 POTENTIAL.  
 CC FT DOMAIN 256 398 CYTOPLASMIC (POTENTIAL).  
 CC FT CAROXYD 81 84 N-LINKED (GLCNAC...?) (POTENTIAL).  
 CC FT CAROXYD 84 84 N-LINKED (GLCNAC...?) (POTENTIAL).  
 CC FT VARSPLIC 63 67 KILVE -> KAMAI (IN ISOFORM 2).  
 CC FT VARSPLIC 68 398 MISSING (IN ISOFORM 2).  
 CC SQ SEQUENCE 398 AA; 43051 MW; 476834B7E7AEC92 CRC64;

Query Match 36.9%; Score 770.5; DB 1; Length 398;  
 Best Local Similarity 49.8%; Pred. No. 8e-46;  
 Matches 142; Conservative 56; Mismatches 84; Indels 3; Gaps 1;

OY 42 MKKRVSTFLVYVYLLIIGAAVFKALEPOEISORTTIVIOKOTIFIAOHACVNSTELDE 101  
 DB 1 MRSTLLALALVALVLSGALVFOALPOHEQOAKKMDHGRDQLRHPVCVSOKSLED 60  
 OY 102 LIQOYVAINAGIIP---LGNSNOVSHMDIGSSFFPAGVITTTIGFNGNSPTTEGGKIF 158  
 DB 61 FIKLLEVALGGGANPETSMNTSSNHSAMMUGSAFFSGITTTIGFNGVLTDTAGRL 120  
 OY 159 CIYVALGIPLEGFLLAGVDDQGTTFGKIAKVEDTFLKMNVSQRIITSTIIFLLG 218  
 DB 121 CIYVALVGIPLFGLMAGVDRGSSLRGIGIHEAIFLKNHPPGLVRSLSAVLELLIG 180  
 OY 219 CULFVALPAVIRKHIKGSALDAIYFVITLTTFGFDYVAGGSDIEYLDYKPVVWMT 278  
 DB 181 CLIFLVTPTFFSYMSWKSLEAIFYIVITLTTFVGFYVPCDGTGQNSPAYQPLVWMT 240  
 OY 279 LVGLAFYAVLSMIGMLVIAKTKEEGGEFRAHAEMTANATA 323  
 DB 241 LRGALFASVLTITGMWLRVSRTRAEWGGITQAASMTGITVA 285

RESULT 5  
 C1W5\_HUMAN  
 ID C1W5\_HUMAN STANDARD; PRT; 499 AA.  
 AC 095279;  
 DT 01-OCT-2000 (rel. 40, Created)  
 DT 01-OCT-2000 (rel. 40, Last sequence update)  
 DT 01-OCT-2000 (rel. 40, Last annotation update)  
 DE POTASSIUM CHANNEL SUBFAMILY K MEMBER 5 (ACID-SENSITIVE POTASSIUM  
 DE CHANNEL PROTEIN TASK-2) (TWIK-RELATED ACID-SENSITIVE K+ CHANNEL 2).  
 GN KCNK5 OR TASK2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_Taxid:9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Kidney;  
 RX MEDLINE-99030343; PubMed-9812978;  
 RA Reyes R., Duprat F., Lesage F., Fink M., Salin P.A., Farnan N.,  
 RA Lazdunski M.;  
 RT Cloning and expression of a novel pH-sensitive two pore domain K+  
 RT channel from human kidney.  
 RL J. Biol. Chem. 273:30863-30869(1998).  
 CC -1- FUNCTION: PH DEPENDENT, VOLTAGE INSENSITIVE, OUTWARDLY RECTIFYING  
 CC POTASSIUM CHANNEL. OUTWARD RECTIFICATION IS LOST AT HIGH EXTERNAL  
 CC K+ CONCENTRATIONS.  
 CC -1- SUBUNIT: HOMODIMER (POTENTIAL).  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).  
 CC -1- TISSUE SPECIFICITY: ABUNDANT EXPRESSION IN KIDNEY, ALSO DETECTED  
 CC IN LIVER, PLACENTA AND SMALL INTESTINE. IN THE KIDNEY, EXPRESSION  
 CC IS RESTRICTED TO THE DISTAL TUBULES AND COLLECTING DUCTS. NOT  
 CC EXPRESSED IN PROXIMAL TUBULES OR GLOMERULI.  
 CC -1- MISCELLANEOUS: INHIBITED BY QUININE, QUINIDINE AND EXTERNAL  
 CC ACIDIFICATION.  
 CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM  
 CC CHANNELS.  
 CC -----  
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 CC -----  
 CC EMBL: AF084830; AAC79458.1; -.  
 CC DR MIM: 603493; -.  
 CC DR InterPro: IPR000099; -.  
 CC DR InterPro: IPR001622; -.  
 CC DR InterPro: IPR003280; -.  
 CC DR Pfam: PR02034; TWIK\_Channel; 1.  
 CC DR PRINTS; PRO1333; 2PORECHANNEL.  
 CC KW Ionic channel; Transmembrane; Ion transport; Potassium transport;  
 CC Glycoprotein.  
 CC FT DOMAIN 1 7  
 CC FT TRANSMEM 8 26 CYTOPLASMIC (POTENTIAL).  
 CC FT DOMAIN 85 112 PORE-FORMING (POTENTIAL).  
 CC FT TRANSMEM 113 133 POTENTIAL.  
 CC FT DOMAIN 134 157 CYTOPLASMIC (POTENTIAL).  
 CC FT TRANSMEM 158 180 POTENTIAL.  
 CC FT DOMAIN 190 215 PORE-FORMING (POTENTIAL).  
 CC FT TRANSMEM 230 250 POTENTIAL.  
 CC FT DOMAIN 251 325 CYTOPLASMIC (POTENTIAL).  
 CC FT CAROXYD 325 375 N-LINKED (GLCNAC...?) (POTENTIAL).  
 CC SQ SEQUENCE 499 AA; 55130 MW; E871A7A4823DDA CRC64;

Query Match 20.1%; Score 420; DB 1; Length 499;  
 Best Local Similarity 30.8%; Pred. No. 8.8e-26;  
 Matches 105; Conservative 62; Mismatches 11; Indels 54; Gaps 11;  
 OY 54 VVLYIIGAAVFKALEPOEISORTTIVIOKOTIFIAOHACVNSTELDELIQOYVAINAG 113



RX MEDLINE-97165959; PubMed-9013852;  
 RA Lesage F., Lautitzen I., Duprat F., Reyes R., Fink M., Heurteaux C.,  
 RA Lazdunski M.;  
 RT "The structure, function and distribution of the mouse TWIK-1 K+  
 RT channel.";  
 RL FEBS Lett. 402:28-32(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-129/SVJ; TISSUE=Liver;  
 RX MEDLINE-98218573; PubMed-9559671;  
 RA Arrighi I., Lesage F., Scimeca J.-C., Carle G.F., Barhanin J.;  
 RT "Structure, chromosome localization, and tissue distribution of the  
 RT mouse twik K+ channel gene.";  
 RL FEBS Lett. 425:310-316(1998).  
 CC -1- FUNCTION: WEAK INWARDLY RECTIFYING POTASSIUM CHANNEL.  
 CC -1- SUBUNIT: HOMODIMER (POTENTIAL).  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).  
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED. HIGHEST EXPRESSION IN BRAIN,  
 CC KIDNEY, THYROID, SALIVARY GLAND, ADRENAL GLAND, PROSTATE,  
 CC EPIDIDYMIS, UTERUS, PLACENTA, COLON AND JEJUNUM, MODERATE  
 CC EXPRESSION IN EYES, PITUITARY, PANCREAS, SMOOTH MUSCLE, TESTIS AND  
 CC OVARY. VERY LOW LEVELS IN LUNG, AORTA, LIVER, HEART, SKELETAL  
 CC MUSCLE, THYMUS AND SPLEEN. IN THE BRAIN, HIGHEST EXPRESSION IN  
 CC CEREBELLAR GRANULE CELLS, BRAINSTEM, HIPPOCAMPUS AND CEREBRAL  
 CC CORTEX.  
 CC -1- DEVELOPMENTAL STAGE: EXPRESSION DETECTED AS EARLY AS 7 DAYS POST  
 CC CONCEPTION. EXPRESSION INCREASES FROM 2-8 DAYS AFTER BIRTH AND  
 CC STABILIZES AFTER DAY 8.  
 CC -1- MISCELLANEOUS: INHIBITED BY QUININE, BARIUM, AND INTERNAL  
 CC ACIDIFICATION. ACTIVATED BY PROTEIN KINASE C.  
 CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM  
 CC CHANNELS.  
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 CC -----  
 DR EMBL AF033017; AAC16973.1; -;  
 DR MGI:109322; Kcni1.  
 DR InterPro: IPR000099; -;  
 DR InterPro: IPR001622; -;  
 DR InterPro: IPR001779; -;  
 DR InterPro: IPR003280; -;  
 DR Pfam: PF02034; TWIK\_channel.1.  
 DR PRINTS: PRO1096; TWIKCHANNEL.  
 DR PRINTS: PRO1335; 2PORECHANNEL.  
 DR Ionic channel; Transmembrane; Ion transport; Potassium transport;  
 KW Glycoprotein.  
 FT DOMAIN 1 20 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 21 41 POTENTIAL.  
 FT DOMAIN 104 130 PORE-FORMING (POTENTIAL).  
 FT TRANSMEM 133 153 POTENTIAL.  
 FT DOMAIN 154 177 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 178 198 POTENTIAL.  
 FT DOMAIN 212 238 PORE-FORMING (POTENTIAL).  
 FT TRANSMEM 247 267 POTENTIAL.  
 FT DOMAIN 268 336 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 95 95 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 336 AA; 38275 MW; A996060A18266FD4 CRC64;

Query Match 17.7%; Score 370; DB 1; Length 336;  
 Best Local Similarity 28.9%; Pred. No. 1,5e-18;  
 Matches 103; Conservative 72; Mismatches 128; Indels 54; Gaps 12;

OY 51 FLVAV--VLYIIIAAFKALPOEISORTTIIYIKOTFIAGHACVNSTLDELIOOIVA 108  
 DB 25 FLVAVGLIIVLVAFAVFSSEELPYEDLLKROELKRLRFLLEHECISEPOLDEOFLGNVLE 84

OY 109 AINAGIIPILGNSSNOVSHMDLGSFFPAGVITITIGFCA--RTREGKIFCIIVALLGIP 168  
 DB 85 ASNVGVSVLSNAGN -WNMFTSALFPASTVLTSTTGCHT--LSDGKACIKIIVSYGIP 143  
 OY 169 LFGELLAGVDQGLTIFGKGLAKVEDFTIKMNSQITIRI--FILPGVLPALP 226  
 DB 144 FTLLFTLALVORIVHYTR--RPVLYPHIRMGFSKOVAIVHVLGLGFTVVSCEFT--P 199  
 OY 227 AVIFKHTE-GMSALDAIFVYITLTITIGFDYVAG-GSDIEYLDYFPVPMFNLVGLAY 284  
 DB 200 AAFVSVLEDDMNFLSEYFPGFISLTIGLDYVPGEGYNKRFELVYKIGTCVLLGLIT 259  
 OY 285 FAVLNMGIMGLVYISKRTKEVEGFRAHAAEWNTANVAEF--TRRLSVEITDKQORAT 344  
 DB 260 MLVVL-----ETCECELHEIK-----KFRKMF 280  
 OY 345 SVRKLSAELAG--NNHDEITPCRRITLVNHLISERVLP--LKAES-ITLNLGTFPH 398  
 DB 281 YVRKDKDEDLVHIMEHDQ-LFSFVVEQVAGLKEEOKSEPFVASOSPPYEDGSADH 336  
 RESULT 8  
 C1M3\_HUMAN  
 ID C1M3\_HUMAN STANDARD; PRT; 394 AA.  
 AC 014649;  
 DT 01-OCT-2000 (Rel. 40, Created)  
 DT 01-OCT-2000 (Rel. 40, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE POTASSIUM CHANNEL SUBFAMILY K MEMBER 3 (ACID-SENSITIVE POTASSIUM  
 DE CHANNEL PROTEIN TASK) (TWIK-RELATED ACID-SENSITIVE K+ CHANNEL).  
 GN KCKN3 OR TASK.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID-9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Kidney;  
 RX MEDLINE-97459932; PubMed-9312005;  
 RA Duprat F., Lesage F., Fink M., Reyes R., Heurteaux C., Lazdunski M.;  
 RT "TASK, a human background K+ channel to sense external pH variations  
 RT near physiological pH.";  
 RL EMBL J. 16:5464-5471(1997).  
 RN [2]  
 RP ACTIVATION.  
 RX MEDLINE-99254548; PubMed-10321245;  
 RA Patel A.J., Honore E., Lesage F., Fink M., Reyes R., Lazdunski M.;  
 RT "Inhalational anesthetics activate two-pore K+ channel in background K+  
 RT channels.";  
 RL Nat. Neurosci. 2:422-426(1999).  
 CC -1- FUNCTION: PH-DEPENDENT, VOLTAGE-INSENSITIVE, BACKGROUND POTASSIUM  
 CC CHANNEL PROTEIN. RECTIFICATION DIRECTION RESULTS FROM POTASSIUM  
 CC ION CONCENTRATION ON EITHER SIDE OF THE MEMBRANE. ACTS AS AN  
 CC OUTWARD RECTIFIER WHEN EXTERNAL POTASSIUM CONCENTRATION IS LOW.  
 CC WHEN EXTERNAL POTASSIUM CONCENTRATION IS HIGH, CURRENT IS INWARD.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).  
 CC -1- TISSUE SPECIFICITY: WIDESPREAD EXPRESSION IN ADULT. STRONGEST  
 CC EXPRESSION IN PANCREAS AND PLACENTA. LOWER EXPRESSION IN BRAIN,  
 CC LUNG, PROSTATE, HEART, KIDNEY, UTERUS, SPINAL INTERSTINE AND COLON.  
 CC -1- MISCELLANEOUS: INHIBITED BY EXTERNAL ACIDIFICATION. ACTIVATED BY  
 CC HALOTHANE AND ISOFLURANE.  
 CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM  
 CC CHANNELS.  
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 CC -----  
 DR EMBL AF006823; AAC51777.1; -;



DR MIM: 603220; -  
 DR InterPro: IPR000099; -  
 DR InterPro: IPR001622; -  
 DR InterPro: IPR003092; -  
 DR InterPro: IPR003280; -  
 DR Pfam: PF02034; TWIK\_channel; 1.  
 DR PRINTS: PRO1095; TASKCHANNEL.  
 DR PRINTS: PRO1333; 2PORECHANNEL.  
 DR Ionic channel; Transmembrane; Ion transport; Potassium transport;  
 KM Glycoprotein.  
 FT DOMAIN 1 8 CYTOPLASMIC (POTENTIAL).  
 FT TRANSSEM 9 29 POTENTIAL.  
 FT DOMAIN 78 101 PORE-FORMING (POTENTIAL).  
 FT TRANSSEM 108 128 POTENTIAL.  
 FT DOMAIN 129 158 CYTOPLASMIC (POTENTIAL).  
 FT TRANSSEM 159 179 POTENTIAL.  
 FT DOMAIN 184 207 PORE-FORMING (POTENTIAL).  
 FT TRANSSEM 223 243 POTENTIAL.  
 FT DOMAIN 244 394 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 53 53 N-LINKED (GLCNAC. .) (POTENTIAL).  
 SO SEQUENCE 394 AA; 43518 MW; 9FAC8266F15FB7 CRC64;

Query Match 17.78; Score 370; DB 1; Length 394;  
 Best Local Similarity 28.08; Pred. No. 1.8e-18;  
 Matches 109; Conservative 66; Mismatches 126; Indels 88; Gaps 13;

QY 42 MKMWTSTIFLV--VYLIIAGAVFAKLEPOEISORTTIVIKOTFIQIACVNS--T 97  
 1 MKRONVTLALIVCTFTYLLVGAIVFDLSEPELIEKORLEKQDELKARYNLSSGGYE 60  
 98 ELDELIOOVAIINAGIIPILGNSSNOVSHMDIGSFEFAGTIVITTFGNSIPRTGGKI 157  
 61 ELEVRVRL-KPHKGV-----QMFAGSFYFAIVITTTIGGHAAPTDGKV 108  
 158 FCITVALGIPFGLAGVDOIGTF-----GKIAYEDTFIKNVSOTMIRI 208  
 109 FCMFYALGIPFLVMOISGERINTLVRLHRAKGLGRRAD-----VSM 156  
 209 ISTIFLFGCVLPAVAFKIHGMSALDAFYVITTTGFGVAGGSD--IEY 266  
 157 ANMWLIGFSCISTLCIGAAAFHYEMTFQAYITTTITGFGDYVALQDQALOT 216  
 267 LDFFKPVWFWILVLAFAVLSMIGDMLRVISKTRKEV----- 307  
 217 QPVYASEFYIILGLVIGAFNLV--VLRFMTNMADEKRAHRLALTRNGAGGG 274  
 308 GEFANHAEMTA-----NTAE-----FKETRRKLSVEL----YDKF 340  
 275 GGGSAHTTDAASSTAAAGGGGFRNVVAEVLHFOGMCSCLMYKREKLQYSIPMIPRDL 334  
 QY 341 QRATSVKRLKSLAELAGNHNOELTPCRTL 369  
 335 TSDTCEVDSHSSPGGGRYSD-TFSKRL 362

RESULT 9  
 C1W3\_MOUSE STANDARD; PRT; 409 AA.  
 AC 03511; 035163;  
 DT 01-OCT-2000 (Rel. 40, Created)  
 DT 01-OCT-2000 (Rel. 40, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE POTASSIUM CHANNEL SUBFAMILY K MEMBER 3 (ACID-SENSITIVE POTASSIUM CHANNEL PROTEIN TASK) (TWIK-RELATED ACID-SENSITIVE K+ CHANNEL)  
 DE CHANNEL PROTEIN TASK (TWIK-RELATED ACID-SENSITIVE K+ CHANNEL)  
 DE CARDIAC TWO-PORE BACKGROUND K+ CHANNEL (CTPAK-1).  
 GN KINK3 OR TASK OR CTBAK.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC TISSUE-Heart;  
 RA MEDLINE=98165556; PubMed=9506712;  
 RA Kim D., Fujita A., Horio Y., Kurachi Y.;  
 RT "Cloning and functional expression of a novel cardiac two-pore  
 RT background K+ channel (CTPAK-1).";  
 RL Circ. Res. 82:513-518(1998).  
 RN [2]  
 RP SEQUENCE OF 4-409 FROM N.A.  
 RX MEDLINE=97459933; PubMed=9312005;  
 RA Duprat F., Lesage F., Fink M., Reyes R., Heurteloux C., Lazdunski M.;  
 RT "TASK, a human background K+ channel to sense external pH variations  
 RT near physiological pH.";  
 RL EMO J. 16:5464-5471(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97459933; PubMed=10748056;  
 RA Lopes C.M., Gallagher P.G., Buck M.E., Butler A.H., Goldstein S.A.;  
 RT "Proton block and voltage gating are potassium-dependent in the  
 RT cardiac leak channel Kcnk3.";  
 RL J. Biol. Chem. 275:16969-16978(2000).  
 CC -1- FUNCTION: PH-DEPENDENT, VOLTAGE-INSENSITIVE, BACKGROUND POTASSIUM  
 CC CHANNEL PROTEIN, RECTIFICATION DIRECTION, RESULTS FROM POTASSIUM  
 CC ION CONCENTRATION ON EITHER SIDE OF THE MEMBRANE. ACTS AS AN  
 CC OUTWARD RECTIFIER WHEN EXTERNAL POTASSIUM CONCENTRATION IS LOW.  
 CC WHEN EXTERNAL POTASSIUM CONCENTRATION IS HIGH, CURRENT IS INWARD  
 CC (BY SIMILARITY).  
 CC -1- SUBUNIT: HOMODIMER (POTENTIAL).  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE; CELL SURFACE; PLASMA  
 CC IN KIDNEY, BRAIN, SKIN, TESTIS, LUNG, SKELETAL MUSCLE, SMALL  
 CC INTESTINE AND STOMACH, NOT DETECTED IN LIVER, THYMUS OR SPLEEN.  
 CC -1- MISCELLANEOUS: INACTIVATED BY BARIUM.  
 CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM  
 CC CHANNELS.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL: AB008537; BAA25436.1; -  
 CC EMBL: AF006824; AAC53367.1; -  
 CC EMBL: AB013345; BAA28349.1; -  
 CC EMBL: AF241798; AAF81418.1; -  
 CC EMBL: AF242508; AAF81418.1; JOINED.  
 CC MDL: MG1:100509; Kcnk3.  
 DR InterPro: IPR000099; -  
 DR InterPro: IPR001622; -  
 DR InterPro: IPR003092; -  
 DR InterPro: IPR003280; -  
 DR Pfam: PF02034; TWIK\_channel; 1.  
 DR PRINTS: PRO1095; TASKCHANNEL.  
 DR PRINTS: PRO1333; 2PORECHANNEL.  
 KW Ionic channel; Transmembrane; Ion transport; Potassium transport;  
 KM Glycoprotein.  
 FT DOMAIN 1 8 CYTOPLASMIC (POTENTIAL).  
 FT TRANSSEM 9 29 POTENTIAL.  
 FT DOMAIN 78 101 PORE-FORMING (POTENTIAL).  
 FT TRANSSEM 108 128 POTENTIAL.  
 FT DOMAIN 129 158 CYTOPLASMIC (POTENTIAL).  
 FT TRANSSEM 159 179 POTENTIAL.  
 FT DOMAIN 184 207 PORE-FORMING (POTENTIAL).  
 FT TRANSSEM 223 243 POTENTIAL.  
 FT DOMAIN 244 409 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 53 53 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CONFLICT 4 4 O -> E (IN REF. 2).  
 FT CONFLICT 123 123 V -> I (IN REF. 2).  
 SO SEQUENCE 409 AA; 45068 MW; 35236E011AAC57 CRC64;

Query Match 16.8%; Score 351; DB 1; Length 409;  
Best Local Similarity 31.1%; Pred. No. 3.7e-17;  
Matches 92; Conservative 61; Mismatches 97; Indels 46; Gaps 10;

QY 42 MKKRTVSTFLVY-VLYLTGAVERKALEPOEISORTIVTOKOTFIACHVNSTEL 99  
DB 1 MKRONRTALIVCTFTYLLVGAADFDALESEPEMIEROLELROLELRARY--NLSEG 57  
QY 100 D-ELIIOIYVAI--NAGIIPLCNSSNOVSHMDLSSFFAGVITITIGNGISPREGG 155  
DB 58 GYELEERVRLRPHKAGV-----QMRPAGSFPAITVITITIGHAPSTDGG 106  
QY 156 KIRCIYIALLGIPFLGVLAVGVDQGTIFGKIAVEDTFIKMNSQTK-----I 206  
DB 107 KVCMEFYALLGIPFLVMEFQSLGERI-----NFFVYILHRAKRGMRHAEV 154  
QY 207 RIISTIFILFGCVLPAVPAVFKHIEGMSALDAIVFVITITIGFGYVAGGSD--1 264  
DB 155 SMANMVLIGFVSCISTLCIGAAAFSYERMTFFOAYVYCTITITIGFGDYVALOKDOAL 214  
QY 265 EYDFFKPVVWFVILVGLAVFAVLSMIGDMLVISKTKTEEGEPRHAAEMTAN 320  
DB 215 QTPQVAFSFFVYILGLTVIGAFNLVY-VLRFMTNMADEKRD-AEHRALLTHN 267

RESULT 10  
C1W3\_RAT STANDARD; PRT: 411 AA.  
ID C1W3\_RAT  
AC 054912:  
DT 01-OCT-2000 (Rel. 40, Created)  
DT 01-OCT-2000 (Rel. 40, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE POTASSIUM CHANNEL SUBFAMILY K MEMBER 3 (ACID-SENSITIVE POTASSIUM CHANNEL PROTEIN TASK) (TWIK-RELATED ACID-SENSITIVE K+ CHANNEL).  
GN KCNK3 OR TASK;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_Taxid=101116;  
RN [1]  
RA TISSUE=Cerebellum;  
RX MEDLINE=98099797; PubMed=9437008;  
RA Leonoudakis D., Gray A.T., Winegar B.D., Kindler C.H., Harada M., Taylor D.M., Chavez R.A., Forsayeth J.R., Yost C.S.;  
RT "An open rectifier potassium channel with two pore domains in tandem cloned from rat cerebellum";  
RL J. Neurosci. 18:868-877(1998).  
CC -1- FUNCTION: PH-DEPENDENT, VOLTAGE-INSENSITIVE, BACKGROUND POTASSIUM CHANNEL PROTEIN. RECTIFICATION DIRECTION RESULTS FROM POTASSIUM ION CONCENTRATION ON EITHER SIDE OF THE MEMBRANE. ACTS AS AN OUTWARD RECTIFIER WHEN EXTERNAL POTASSIUM CONCENTRATION IS LOW. WHEN EXTERNAL POTASSIUM CONCENTRATION IS HIGH, CURRENT IS INWARD (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).  
CC -1- TISSUE SPECIFICITY: STRONGEST EXPRESSION IN HEART. MODERATE EXPRESSION IN LUNG AND BRAIN. LOW LEVELS IN LIVER, KIDNEY AND SKELETAL MUSCLE.  
CC -1- MISCELLANEOUS: INHIBITED BY EXTRACELLULAR ACIDIFICATION, ZINC, BUTYRACIN AND PHENOTOIN. ACTIVATED BY PROTEIN KINASE A.  
CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM CHANNELS.  
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CC EMBL: AF031384; AAC39952.1; -  
CC InterPro: IPR000099; -

DR InterPro: IPR001622; -  
DR InterPro: IPR003092; -  
DR InterPro: IPR003280; -  
DR Pfam: PF02034; TWIK\_channel; 1.  
DR PRINTS: PR01095; TASKCHANNEL.  
DR PRINTS: PR01333; 2PORECHANNEL.  
KW Ionic channel; Transmembrane; Ion transport; Potassium transport; Glycoprotein.  
FT DOMAIN 1 8 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 9 29 POTENTIAL.  
FT DOMAIN 78 101 PORE-FORMING (POTENTIAL).  
FT TRANSMEM 108 128 POTENTIAL.  
FT DOMAIN 129 158 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 159 179 POTENTIAL.  
FT DOMAIN 184 207 PORE-FORMING (POTENTIAL).  
FT TRANSMEM 223 243 POTENTIAL.  
FT DOMAIN 244 411 CYTOPLASMIC (POTENTIAL).  
FT CARBOHYD 53 53 N-LINKED (GLCNAC) (POTENTIAL).  
SQ SEQUENCE 411 AA; 45276 MW; D2778016E09E215 CRC64;

Query Match 16.8%; Score 351; DB 1; Length 411;  
Best Local Similarity 31.1%; Pred. No. 3.7e-17;  
Matches 92; Conservative 61; Mismatches 97; Indels 46; Gaps 10;

QY 42 MKKRTVSTFLVY-VLYLTGAVERKALEPOEISORVITITIGFGNISPTREG 155  
DB 1 MKRONRTALIVCTFTYLLVGAADFDALESEPEMIEROLELRLARY--NLSEG 57  
QY 100 D-ELIIOIYVAI--NAGIIPLCNSSNOVSHMDLSSFFVITITIGFGNISPTREG 155  
DB 58 GYELEERVRLRPHKAGV-----QMRPAGSFVITITIGFGHAPSTDGG 106  
QY 156 KIRCIYIALLGIPFLGVLAVGVDQGTIFGKIAVEVKNNSQTK-----I 206  
DB 107 KVCMEFYALLGIPFLVMEFQSLGERI-----NFFVYILHRAKRGMRHAEV 154  
QY 207 RIISTIFILFGCVLPAVPAVFKHIEGMSALDAIVITITIGFGDYVAGGSD--1 264  
DB 155 SMANMVLIGFVSCISTLCIGAAAFSYERMTFFOAYVYCTITITIGFGDYVALOKDOAL 214  
QY 265 EYDFFKPVVWFVILVGLAVFAVLSMIGDMLVISKTKTEEGEPRHAAEMTAN 320  
DB 215 QTPQVAFSFFVYILGLTVIGAFNLVY-VLRFMTNMADEKRD-AEHRALLTHN 267

RESULT 11  
C1W6\_HUMAN STANDARD; PRT: 313 AA.  
ID C1W6\_HUMAN  
AC Q9Y257;  
DT 01-OCT-2000 (Rel. 40, Created)  
DT 01-OCT-2000 (Rel. 40, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE POTASSIUM CHANNEL SUBFAMILY K MEMBER 6 (INWARD RECTIFYING POTASSIUM CHANNEL PROTEIN TWIK-2) (TWIK-ORIGINATED SUBFAMILY SEQUENCE).  
GN KCNK6 OR TWIK2 OR TOSS.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RA TISSUE=Testis;  
RX MEDLINE=99285568; PubMed=10359073;  
RA Pountney D.J., Gulkarov I., Vega-Saenz de Maza E., Holmes D., Sagantich M., Rudy B., Artman M., Coetzee W.;  
RT "Identification and cloning of TWIK-Origins (TOSS): a novel human 2-pore K+ channel protein with a subunit";  
RL FEBS Lett. 450:191-196(1999).  
RN [2]  
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF CYS-122 IN TWIK-2;  
RC TISSUE=Brain;  
RX MEDLINE=99175162; PubMed=10075682;

RA Chavez R.A., Gray A.T., Zhao B.B., Kindler C.H., Mazurek M.J.,  
 RA Mehta Y., Forsayeth J.R., Yost C.S.,  
 RT "TWIK-2, a new weak inward rectifying member of the tandem pore domain  
 RT potassium channel family." J. Biol. Chem. 274:7887-7892(1999).  
 RN [3]  
 RP ERRATUM.  
 RA Chavez R.A., Gray A.T., Zhao B.B., Kindler C.H., Mazurek M.J.,  
 RA Mehta Y., Forsayeth J.R., Yost C.S.,  
 RL J. Biol. Chem. 274:24440-24440(1999).  
 CC -1- FUNCTION: WEAK INWARDLY RECTIFYING POTASSIUM CHANNEL.  
 CC -1- SUBUNIT: HOMODIMER (POTENTIAL)  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).  
 CC -1- TISSUE SPECIFICITY: WIDESPREAD EXPRESSION, DETECTED IN ALL TISSUES  
 CC TESTED EXCEPT FOR SKELETAL MUSCLE. STRONGEST EXPRESSION IN  
 CC PLACENTA, PANCREAS, HEART, COLON AND SPLEEN, LOWER LEVELS DETECTED  
 CC IN PERIPHERAL BLOOD LEUCOCYTES, LUNG, LIVER, KIDNEY AND THYMUS.  
 CC LOWEST EXPRESSION DETECTED IN BRAIN.  
 CC -1- MISCELLANEOUS: INHIBITED BY INTERNAL ACIDIFICATION AND, TO A SMALL  
 CC DEGREE, BY ZINC. NOT INHIBITED BY QUININE, QUINIDONE OR BARBITUM.  
 CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM  
 CC CHANNELS.  
 CC -----  
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 CC -----  
 DR EMBL: AF134149; AAD22980.1; -;  
 DR EMBL: AF117708; AAD24000.1; -;  
 DR MIM: 603939; -;  
 DR InterPro: IPR001622; -;  
 DR InterPro: IPR001779; -;  
 DR PRINTS: PRO1096; TWIKCHANNEL.  
 DR Ionic channel; Transmembrane; Ion transport; Potassium transport;  
 KW Glycoprotein.  
 FT DOMAIN 1 4 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 5 25 POTENTIAL.  
 FT DOMAIN 90 115 PORE-FORMING (POTENTIAL).  
 FT TRANSMEM 121 141 POTENTIAL.  
 FT DOMAIN 142 172 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 173 193 POTENTIAL.  
 FT DOMAIN 199 223 PORE-FORMING (POTENTIAL).  
 FT TRANSMEM 236 256 POTENTIAL.  
 FT DOMAIN 257 313 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 79 79 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 85 85 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT NOTAGN 53 53 C->A: NO CHANNEL ACTIVITY.  
 SQ SQUENCE 313 AA; 33747 MW; 1379382DFB0575DE CRC64;

Query Match 16.4%; Score 342; DB 1; Length 313;  
 Best Local Similarity 34.4%; Pred. No. 1.1e-16;  
 Matches 83; Conservative 42; Mismatches 104; Indels 12; Gaps 5;

QY 57 YLITGAFALEAEPQESITTIIVIOKOTIFIAQHACVNSTEDELIIQOYVATNAGIIP 116  
 DB 17 YLVIGALLVRLLEGPHARARAELETRRAOLRSPCVAPADAFERYVLAAGRLGRV 76  
 QY 117 LGNSNNOVS---HMDGSSFFAGVITITIGFNGISPRTEGGKIFCIIVALLGIPLEGF 172  
 DB 77 LANSSGANSNDPAMDASALFFPASTITITVGYCTTPLDAGCAFIARLLGCVPTTML 136  
 QY 173 LLAGVGDLGTTEGKIAKVEDFFIKWNSQFKIRIITIIIFLFGCVLEVA--LPAVIF 230  
 DB 137 LITFASARLSTL---LTHVPLSLWLSMRMGWDPBRACAMHLVALLGVVTVVTCFLPVAVIF 192  
 QY 231 KHI-EGMSALDAIYFVYITITITIGFGDYVAGSGDIE-YLDFYKRVVWFWILGLATYRAAV 288  
 DB 193 AHLEEASFLDAFYCFISLSTIGLDGYVPGEAGOPYRALYKVLVTVYVYFLGLVAVLV 252

QY 289 L 289  
 DB 253 L 253

RESULT 12  
 ORK1\_DROME STANDARD; PRT; 1001 A;  
 ID ORK1\_DROME 094526;  
 AC 094526;  
 DT 01-OCT-2000 (Rel. 40, Created)  
 DT 01-OCT-2000 (Rel. 40, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE OPEN RECTIFIER POTASSIUM CHANNEL PROTEIN 1 (A TWO PORE DOMAIN POTASSIUM  
 DE CHANNEL ORK1).  
 GN ORK1 OR CG1615.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Schizophora; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_Taxid=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Larva.  
 RX MEDLINE=97075152; PubMed=8917578;  
 RA Goldstein S.A.N., Price L.A., Rosenthal D.N., Busch M.H.,  
 RT "ORK1, a potassium-selective leak channel with two pore domains  
 RT cloned from Drosophila melanogaster by expression in Saccharomyces  
 RT cerevisiae." Proc. Natl. Acad. Sci. U.S.A. 93:13256-13261(1996).  
 RL [2]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=BERKELEY;  
 RC MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoek R.R., Galie R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers J.H., Blazer R.G., Olmpe M., Pfeiffer B.D.,  
 RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abell J.F., Agbayani A., An H.-J., Andrews L., Binkov C., Baldwin D.,  
 RA Bailew R.M., Basu A., Baxendale J., Bayraktar S.L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhand J., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,  
 RA Burris K.C., Busam D.A., Butler H., Cadieu I., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport J., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha J., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrara S., Fleischmann W.,  
 RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei K.-H., Ideyem C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kevinson J.A., Kelchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lascko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Matrei B., McIntosh T.C., McLeod M., McPherson D.,  
 RA Merklov G., Mishina N.V., Moberg C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Wu D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
 RA Palazolo M., Pittman G.S., Pan S., Pollard D., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheer F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Sotter E., Spradling A.C., Stapleton M., Strick R., Sun E.,  
 RA Stykasz R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu L., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster." Science 287:2185-2195(2000).  
 RL -1- FUNCTION: BACKGROUND POTASSIUM CHANNEL. RECTIFICATION IS DEPENDENT

ON EXTERNAL POTASSIUM CONCENTRATION. ACTS AS AN OUTWARDLY  
RECTIFYING CHANNEL BUT AS EXTERNAL POTASSIUM LEVELS INCREASE, THIS  
IS REVERSED.

-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).  
-1- TISSUE SPECIFICITY: WIDESPREAD EXPRESSION IN ADULT, STRONGEST  
EXPRESSION IN MUSCLE, BRAIN AND OVARY. ALSO PRESENT AT LOW LEVELS  
IN LARVA AND EMBRYO.

-1- MISCELLANEOUS: INHIBITED BY BARIUM.  
-1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM  
CHANNELS.

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CC  
CC  
CC EMBL; U55321; AAC69250.1; -  
CC FLYBASE; FBgn0017561; OTK1.  
CC InterPro; IPR000009; -  
CC InterPro; IPR001622; -  
CC InterPro; IPR003280; -  
CC Pfam; PF00234; TWIK channel; 1.  
CC PRINTS; PR01333; 2PORECHANNEL.  
CC DR  
CC Ionic channel; Transmembrane; Ion transport; Potassium transport;  
CC Glycoprotein.  
CC KW  
CC DOMAIN 1 6 CYTOPLASMIC (POTENTIAL).  
CC FT TRANSMEM 7 27 POTENTIAL.  
CC FT DOMAIN 95 111 PORE-FORMING (POTENTIAL).  
CC FT TRANSMEM 120 140 POTENTIAL.  
CC FT DOMAIN 141 170 CYTOPLASMIC (POTENTIAL).  
CC FT TRANSMEM 171 191 POTENTIAL.  
CC FT DOMAIN 208 224 PORE-FORMING (POTENTIAL).  
CC FT TRANSMEM 244 264 POTENTIAL.  
CC FT DOMAIN 265 1001 CYTOPLASMIC (POTENTIAL).  
CC FT CARBOHYD 58 58 N-LINKED (GLYCANC. .) (POTENTIAL).  
CC FT  
CC SEQUENCE 1001 AA; 109289 MW; 09A1A1A669072E07 CRC64;

Query Match 15.6%, Score 325, DB 1, Length 1001;  
Best Local Similarity 28.8%, Pred. No. 5.7e-15;  
Matches 90; Conservative 62; Mismatches 125; Indels 36; Gaps 10;

OY 50 IFLVVVLLIIGANFKLEQPOE-----ISQTTIVIKQPIAQAACVNSFELDELQO 105  
DB 9 LLIPISTILMGAAIYIYHIEGEEKISRAQKAOIAINEYILLEELGDKNTTODEILQR 68  
OY 106 IVAAINAGIILPGNSSNOVSHMDLSSSEFFAGTVITTTIGFNISIPRTSGKIFCIYVAL 165  
DB 69 ISDYCDKRVTLPPYVDPIRYTWTFYHAFEPFAVTCSTGYGMSIPSTFGGRIMIAYSVI 128  
OY 166 GIPFLGFLLAGYGOGLGITFGKGIKAKVEDTEPKMNV-----QTKIRIISTIFILP-G 218  
DB 129 GIPVNGIIFAG---LGEFGRFEPFAIYRKYKKKMSDMMHYVPPOGLITVTVALIPG 184  
OY 219 CVLPALPAVIFKHIEGMSALDAIYFVVITLTITGFGYVA-----CGSDIEYLD 268  
DB 185 IALFLFLDSWFTFYENNPYSISLKYVYVTTTITGFGDVLPFTFGANOPKREFGMVFYQI 244  
OY 269 FYKPVVWVWILVGLAYFAVLISMIGDWLRVITSK-----TKEEVGFRFAHAEMTANVTA 324  
DB 245 FV--IVWE--IFSGDYLVMIWMTFIRGLQ--SKRLATYLEQGLSSNLKATPNKINMSGVTRKD 298  
OY 325 FKETRLRLSVELY 337  
DB 299 VGYLRRLN-ELY 310

ID C1W8\_MOUSE STANDARD: PR1: 307 AA.  
 AC 092211; Q9R242; Q9R1V1; Q9QYB6; Q9QX010;  
 DT 01-OCT-2000 (Rel. 40, Created)  
 DT 01-OCT-2000 (Rel. 40, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE POTASSIUM CHANNEL SUBFAMILY K MEMBER 8 (PUTATIVE POTASSIUM CHANNEL DP3) (DOUBLE-PORE K+ CHANNEL 3) (NEURONOSCULAR TWO P DOMAIN POTASSIUM CHANNEL).  
 DE KCNK8 OR KCNKG OR DPKH3 OR KNOT1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain, and Lung;  
 RX MEDLINE=99223496; PubMed=10206991;  
 RA Salinas M., Reyes R., Lesage F., Fosset M., Heurteaux C., Romey G., Lazdunski M.;  
 RT "Cloning of a new mouse two-P domain channel subunit and a human homologue with a unique pore structure";  
 RL J. Biol. Chem. 274:11751-11760(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Ishibashi K., Suzuki M., Imai M.;  
 RT "Cloning of a new double-pore K channel expressed predominantly in testis";  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE OF 1-289 FROM N.A.  
 RA Bockenhauer D., Nimakayala M.A., Ward D.C., Goldstein S.A.N., Gallagher P.G.;  
 RT "Cloning, localization, and expression of the human 2 P domain potassium channel KCNKG.";  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE OF 2-307 FROM N.A.  
 RA Gan L., Joiner W.J., Quinn A.M., Wang L.-Y., Gates T., Kaczmarek L.K.;  
 RT Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE OF 15-307 FROM N.A.  
 RC TISSUE=Brain;  
 RA Lopes C.M.B., Buck M., Goldstein S.A.N.;  
 RT "A new two P domain potassium channel subfamily from mouse excitable tissues";  
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: PROBABLE POTASSIUM CHANNEL SUBFAMILY K MEMBER 8. CHANNEL ACTIVITY OBSERVED IN VITRO AS PROTEIN REMAINS IN THE CYTOSOLIC RETICULUM. MAY NEED TO ASSOCIATE WITH AN AS YET UNKNOWN PARTNER IN ORDER TO REACH THE PLASMA MEMBRANE.  
 CC -1- SUBUNIT: HOMODIMER (POTENTIAL).  
 CC -1- TISSUE SPECIFICITY: DETECTED IN EMBRYO, LUNG AND LIVER, WEAKLY EXPRESSED IN COLON, TESTIS, ATRIAL MYOCYTES AND BRAIN STEM. NOT DETECTED IN BRAIN, CEREBELLUM, SPINAL CORD, HEART, VENTRICLE, SKELETAL MUSCLE, LIVER, PLACENTA AND PANCREAS. IN THE EYE, HIGHLY EXPRESSED IN THE RETINAL GANGLION CELL LAYER AND INNER NUCLEAR LAYER.  
 CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM CHANNELS.  
 CC -----  
 CC THIS SWISS-PROT entry is copyright. It is provided through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Use by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL, AF110521; AAD29577.1; ALT\_TERM.  
 CC EMBL, AB015729; BAA35074.1; -  
 CC EMBL, AF022820; AAD09337.1; -  
 CC

Query Match	14.6%	Score 305.5	DB 1	Length 307
Best Local Similarity	29.6%	Pred. No. 3.5e-14		
Matches 84	Conservative 65	Mismatches 94	Indels 41	Gaps 12

	RESULT	14
CIW7_HUMAN		
ID	CIW7_HUMAN	STANDARD;
AC	O9Y2U2; O9Y2U4; O9Y2U3;	PRT; 307 AA.
DT	01-OCT-2000 (Rel. 40, Created)	
DT	01-OCT-2000 (Rel. 40, Last sequence update)	
DT	01-OCT-2000 (Rel. 40, Last annotation update)	
DE	POTASSIUM CHANNEL SUBFAMILY K MEMBER 7.	
GN	KCNK7.	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Euthelia; Plimates; Catarrhini; Homiidae; Homo.	
OX	NCBI_TaxID=9606;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RP	TISSUE=Brain;	
RX	MEDLINE=99223496; PubMed=10206991;	
RA	Salinas M., Reyes R., Lesage F., Fosset M., Heurteaux C., Romey G.,	
RA	Lardunski M.;	
RT	"Cloning of a new mouse two-P domain channel subunit and a human	
RT	homologue with a unique pore structure.";	

ID	Name	Accession	Length	Description
DR	EMBL; AF110522;	AAD29578.1;	-	
DR	EMBL; AF110524;	AAD29580.1;	-	
DR	EMBL; AF110523;	AAD29579.1;	-	
DR	MIM: 603940;	-	-	
DR	InterPro: IPR001622;	-	-	
KW	Ionic channel; Transmembrane; Ion transport; Assay transport;			
KM	Glycoprotein; Alternative splicing.			
FT	DOMAIN	1	10	CYTOPLASMIC (POTENTIAL).
FT	TRANSSEM	11	31	POTENTIAL.
FT	DOMAIN	92	119	PORE-FORMING (POTENTIAL).
FT	TRANSSEM	120	140	POTENTIAL.
FT	DOMAIN	141	170	CYTOPLASMIC (POTENTIAL).
FT	TRANSSEM	171	191	POTENTIAL.
FT	DOMAIN	199	227	PORE-FORMING (POTENTIAL).
FT	TRANSSEM	233	253	POTENTIAL.
FT	DOMAIN	254	307	CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	83	83	N-LINKED (GLCNAC... ) (POTENTIAL).
FT	VARSPLIC	241	252	YLGLGLAMLA -> GTSISLGATWEIG (IN ISOFORM B).
FT	VARSPLIC	253	307	MISSING (IN ISOFORM B).
FT	VARSPLIC	241	257	YLGLGLAMLAVERTS -> KSHSLTACGGRGRSLSD (IN ISOFORM C).
FT	VARSPLIC	258	307	MISSING (IN ISOFORM C).
SO	SEQUENCE	307 AA:	31946 MW:	BDA436DD9591AD <sup>TM</sup> CRC64;

Query Match	14.4%	Score 300.5	DB: NCBI	Length 307
Best Local Similarity	29.9%	Pred. No. 7,66-14		
Matches	88	Conservative	60	Mismatches 111
			Indels	35
			Gaps	10

  

QY	44	WKVSTIFLVVVLVLLIGAAVFKALEDPQEIISORTIVICK	PIAQH-ACVNSTELDEL	102
		: : : : :   : : : : :   : : : : :   : : : : :		
DY	7	MSRVGLLVVAHLLLGAAVVFQALEGPPACRLQALELNAEI	VQAEHRACLPCGALBEL	66
QY	103	IQQIVAAINAGIIPLGNSNOVSHMDLGSSEFFACTVITTTGKINSIPRTBGGKIFCIIT		162
		: : : : :   : : : : :   : : : : :   : : : : :		
DY	67	LGTALAQAHGVSTLGNSS-EGRTMDLPESALLFAASILIT	YGHMPLSPGKAFCMY	125
QY	163	ALLGIPLEGELLAGQDGTIFPGKIKKVEDTEFKMNV	YKINISITIFILEGCULF	222
		: : : : :   : : : : :   : : : : :   : : : : :		
DY	126	AAIGIPASLAVATLRHCLRPVLSKPRMVA--VHWOL	SEVARAALLDAVALGLLVASSF	182
QY	223	VALPAVIFKHIEG-MSALDAIYFVVTITTTIGFGDYVAG	GSDIEYLDPYKPVVWF----	276
		: :		
DY	183	VLPALVYIMGIGQCSLIGAVYFCFSSLSITIGEDLLPG	RSLSH-----PVYIHLQDL	236
QY	277	---:WILVGLAYFAAVISMIGDWLRLVISKTKKEYVEGFR	IIAAEW--TANVTAE	324
		: : : : :   : : : : :   : : : : :   : : : : :		
DY	237	ALTGYLLGLL-----LAML-----LAVETSELD	PQYRAKCKFRRPGPVTAE	278





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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 28, 2001, 17:12:45 ; Search time 54.36 Seconds  
(without alignments)  
1000.319 Million cell updates/sec

Title: US-09-503-089a-4  
Perfect score: 2090  
Sequence: 1 MAAPDLDPKSAQNSKPRRL.....LNGLTPHCAGEDIAVENMK 411

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues  
Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: SPREMBL\_16:\*  
2: SP\_archaea:\*  
3: SP\_bacteria:\*  
4: SP\_fungi:\*  
5: SP\_human:\*  
6: SP\_invertebrate:\*  
7: SP\_mammal:\*  
8: SP\_mhc:\*  
9: SP\_organellar:\*  
10: SP\_phage:\*  
11: SP\_plant:\*  
12: SP\_rodent:\*  
13: SP\_unclassified:\*  
14: SP\_vertebrate:\*  
15: SP\_virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2044	97.8	411	4 Q9NRT2	Q9NRT2 homo sapien
2	1256.5	60.1	4	Q9JIS4	Q9JIS4 rattus norv
3	1251.5	59.9	4	Q9HBS9	Q9HBS9 homo sapien
4	499.5	23.9	4	Q9H591	Q9H591 homo sapien
5	409	19.6	502	11 Q9TK62	Q9TK62 mus musculu
6	375.5	18.0	336	11 Q9ZT2	Q9ZT2 rattus norv
7	351.5	16.9	259	6 Q02821	Q02821 oryctolagus
8	351.5	16.8	330	4 Q9HBC8	Q9HBC8 homo sapien
9	351.5	16.8	365	11 Q9JLS8	Q9JLS8 cavia porce
10	344	16.5	289	11 Q9QX34	Q9QX34 mus musculu
11	343.5	16.4	330	4 Q9H427	Q9H427 homo sapien
12	343	16.4	329	5 Q76795	Q76795 caenorhabd
13	342.5	16.4	374	4 Q9NPC2	Q9NPC2 homo sapien
14	338.5	16.2	229	4 Q9H592	Q9H592 homo sapien
15	338	16.2	313	11 Q9ERU5	Q9ERU5 rattus norv
16	335	16.0	395	11 Q9JLUD4	Q9JLUD4 rattus norv
17	329.5	15.8	336	5 Q17185	Q17185 caenorhabd
18	322.5	15.4	237	11 Q9ES08	Q9ES08 rattus norv
19	309.5	14.8	343	11 Q9JL14	Q9JL14 mus musculu

20	308.5	14.8	430	4 Q9HBI5	Q9HBI5 homo sapien
21	307	14.7	430	11 Q9ERS1	Q9ERS1 rattus norv
22	306	14.6	340	5 Q9VHE0	Q9VHE0 drosophila
23	304.5	14.6	398	5 Q9VRS9	Q9VRS9 drosophila
24	294.5	14.1	392	11 Q9ERS5	Q9ERS5 rattus norv
25	289	13.8	383	5 Q21094	Q21094 caenorhabd
26	287	13.7	405	11 Q9ERS0	Q9ERS0 rattus norv
27	286.5	13.7	364	5 Q76790	Q76790 caenorhabd
28	284	13.6	385	5 Q9VYX5	Q9VYX5 drosophila
29	279.5	13.4	408	4 Q9HBI4	Q9HBI4 homo sapien
30	279.5	13.4	461	5 Q9TZP8	Q9TZP8 caenorhabd
31	279	13.3	393	5 Q9XU07	Q9XU07 caenorhabd
32	271	13.0	392	5 Q9NEV3	Q9NEV3 caenorhabd
33	270.5	12.9	522	5 Q22042	Q22042 caenorhabd
34	269	12.9	325	5 Q18120	Q18120 caenorhabd
35	266	12.7	1910	5 Q22426	Q22426 caenorhabd
36	263	12.6	452	5 Q93531	Q93531 caenorhabd
37	256.5	12.3	395	5 Q9V362	Q9V362 drosophila
38	252.5	12.1	1539	5 Q19611	Q19611 caenorhabd
39	247	11.8	444	5 Q45891	Q45891 caenorhabd
40	246	11.8	389	5 Q9VE68	Q9VE68 drosophila
41	245.5	11.7	513	5 Q22940	Q22940 caenorhabd
42	244.5	11.7	270	11 Q9JL57	Q9JL57 cavia porce
43	243.5	11.7	427	5 Q23386	Q23386 caenorhabd
44	237	11.3	643	5 Q9XXF6	Q9XXF6 caenorhabd
45	236	11.3	550	5 Q93764	Q93764 caenorhabd

## ALIGNMENTS

RESULT 1  
Q9NRT2 PRELIMINARY: PRT; 411 AA.  
ID Q9NRT2  
AC Q9NRT2  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE TWO-PORE DOMAIN POTASSIUM CHANNEL TREK-1.  
GN TREK-1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BRAIN;  
RA Meadows H.J., Benham C.D., Cairns W., Gloger J.S., Jennings C.,  
RA Medhurst A.D., Murdock P., Chapman C.G.;  
RT "Cloning, localization and functional expression of the human ortholog  
of the TREK-1 potassium channel."  
RL Submitted (Jul-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF171068; AAF89743.1;  
DR InterPro: IPR001622;  
DR InterPro: IPR003280;  
DR PRINTS: PR01333; ZP0REKCHANEL.  
KW Ionic channel.  
SQ SEQUENCE 411 AA; 45494 MW; FDE40CAB21B42; CRC64;

Query Match 97.8%; Score 2044; DB Length 411;  
Best Local Similarity 96.4%; Pred. No. 1e-11;  
Matches 396; Conservative 11; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MAAPDLDPKSAQNSKPRLSFSKPTVLASRVESDSAINWKYVSTFLVYVLLIT 60  
DB 1 MAAPDLDPKSAQNSKPRLSFSKPTVLASRVESDITINWAKYVSTFLVYVLLIT 60  
QY 61 GAIVFALKEQPELSEQFTVIOKQFIQAHCNSLELLELQIVAAINAGIIPGNS 120  
DB 61 GAIVFALKEQPELSEQFTVIOKQFIQAHCNSLELLELQIVAAINAGIIPGNT 120  
QY 121 SNQVSHMDLSSFFFACTVITIGFGNISPRTEGKITFIVALGIPFGFLAGVGDQ 180

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Db 121 SNQSHWMDGSSFFAGVYITTTIGFNGISPRTEGKIFCIITAYALGIPLEFGLAAVGQ 180
QY 181 LGTIGKGIKAKVEDPFIKNNVSOTKIRIISTITFIIFGCVLPAVALPAVFKHIEGSAID 240
Db 181 LGTIFGKGIKAKVEDPFIKNNVSOTKIRIISTITFIIFGCVLPAVALPAVFKHIEGSAID 240
QY 241 AITFVYITLTITGFDYVAGSGDIEYLDYKPPVPMFIIIVGLAFPAVSMIGDMIRVTS 300
Db 241 AITFVYITLTITGFDYVAGSGDIEYLDYKPPVPMFIIIVGLAFPAVSMIGDMIRVTS 300
QY 301 KKTKEVGEFRAHAAEMWTANTAEFEKTRRLSVEIYDKFORATSVKRLSALAGNHQ 360
Db 301 KKTKEVGEFRAHAAEMWTANTAEFEKTRRLSVEIYDKFORATSVKRLSALAGNHQ 360
QY 361 ELTPCRRITSVNHLTSEREVLPPLKASITLYNGLTPHRCAGEDIAVIEWK 411
Db 361 ELTPCRRITSVNHLTSEREVLPPLKASITLYNGLTPHRCAGEDIAVIEWK 411

```

## RESULT 2

```

Q9JIS4 PRELIMINARY: PRT: 538 AA.
ID 09JIS4
AC 09JIS4;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, last annotation update)
DE POTASSIUM CHANNEL TREK-2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20298807; PubMed=10747911;
RA Bang H., Kim Y., Kim D.;
RT "TREK-2, a new member of the mechanosensitive tandem-pore K+ channel
RT family.";
RT J. Biol. Chem. 275:17412-17419(2000).
DR EMBL: AF196965; AAF5132.1; -.
DR InterPro: IPR000099; -.
DR InterPro: IPR001622; -.
DR InterPro: IPR003280; -.
DR Pfam: PF02034; TWIK_channel; 1.
DR PRINTS: PR01333; 2PORECHANNEL.
SQ SEQUENCE 538 AA: 59800 MW: 1FF33F0AA52B97E4 CRC64:

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Query Match 60.1%; Score 1256.5; DB 11; Length 538;  
 Best Local Similarity 65.3%; Pred. No. 1, 1e-83;  
 Matches 247; Conservative 55; Mismatches 65; Indels 11; Gaps 5;

```

QY 2 AAPDLDPKSA--AONSKRLSPSSKPYVLASVESDS--AINWKKMTVSTIPLVYV 56
Db 23 AAPVQCPKSAATNGHPRLSISRAIYVA-RMEGASOGGLOTQVKKMTVAIFVYVV 81
QY 57 YLIGAAVKALEQPOEISORTTIVIOKQFTIAQHACVSTELDELIOQVAIAINAGIIP 116
Db 82 YLVTGGLVRALEQPESSOKNTIALEKAEFLDHCVSQOELETLIOHALDNGVSP 141
QY 117 LGNSSQVSHWMDGSSFFAGVYITTTIGFNGISPRTEGKIFCIITAYALGIPLEFGLAG 176
Db 142 VGNSSSSSHWMDGSAFFAGVYITTTIGFNGIAPSPGEGKIFCIITAYALGIPLEFGLAG 201
QY 177 VGDQLTITGKGIKAKVEDPFIKNNVSOTKIRIISTITFIIFGCVLPAVALPAVFKHIEG 236
Db 202 IGDLGTITGKGIKAKVEDPFIKNNVSOTKIRIISTITFIIFGCVLPAVALPAVFKHIEG 261
QY 237 SALDAITFVYITLTITGFDYVAG--SDIEYLDYKPPVPMFIIIVGLAFPAVSMIGDM 295
Db 262 TALESTIFVYVITLTITGFDYVAGGAGNAGINREMYKPLVWMTLVGLAFPAVSMIGDM 321
QY 296 LRVISKRTKEVGEFRAHAAEMWTANTAEFEKTRRLSVEIYDKFORATSV---RKLS 351

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Db 322 LRVLSKRTKEVGEIKAHAAEMKANTAEFRTRRLSV--MDIKQIRATISMERRRLG 381
QY 352 AELAGNHNOELTPCRRTL 369
Db 382 LDQRAHSLDMLSPKRSV 399

```

## RESULT 3

```

Q9HB59 PRELIMINARY: PRT: 538 AA.
ID 09HB59
AC 09HB59;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, last annotation update)
DE 2P DOMAIN POTASSIUM CHANNEL TREK2.
GN KCNK10.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20435789; PubMed=10880510;
RA Lesage F., Terrenoire C., Romey G., Lazdunski L.;
RT "Human TREK2, a 2P domain mechano-sensitive K+ channel with multiple
RT regulations by polyunsaturated fatty acids, 1,3-phospholipids and Gs,
RT Gi, and Gq protein-coupled receptors.";
RT J. Biol. Chem. 275:28398-28405(2000).
DR EMBL: AF279890; AAG5191.1; -.
KW Ionic channel.
SQ SEQUENCE 538 AA: 59764 MW: 8EA615B08D147FE CRC64:

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Query Match 59.9%; Score 1251.5; DB 1; Length 538;  
 Best Local Similarity 64.3%; Pred. No. 2, 5e-83;  
 Matches 247; Conservative 54; Mismatches 61; Indels 17; Gaps 5;

```

QY 2 AAPDLDPKSA-----AONSKRLSPSSKPYVLASVE--S--AINWKKMTVSTI 50
Db 17 AAPVQCPKSAATNGPPAPAPPTPRLSISRAIYVA-RME--VSGGLOTQVKKMTVAI 75
QY 51 FLVVVLYLTIGAAVKALEQPOEISORTTIVIOKQFTIAQHACVSTELDELIOQVAI 110
Db 76 FLVVVLYLTIGVLRALQPESSOKNTIALEKAEFLDHCVSQOELETLIOHALDAD 135
QY 111 NAGIIPLGNSQVSHWMDGSSFFAGVYITTTIGFNGISF--GKIFCIITAYALGIPLE 170
Db 136 NAGVSPITGNSNNSSSHWMDGSAFFAGVYITTTIGFNGIAP--VGGKIFCIITAYALGIPLE 195
QY 171 GFLLAGVGQDLTITGKGIKAKVEDPFIKNNVSOTKIRIIS--FIIFGCVLPAVALPAV 230
Db 196 GFLLAGIGQDLTITGKGIKAKVEDPFIKNNVSOTKIRIIS--FIIFGCVLPAVALPAV 255
QY 231 KHIEGSAIDAITFVYITLTITGFDYVAG--SDIEYLDYKPPVPMFIIIVGLAFPAVL 289
Db 256 KTIIEGTALESITFVYVITLTITGFDYVAGGAGNAGINREMYKPLVWMTLVGLAFPAVL 315
QY 290 SMIGDMIRVTSKRTKEVGEFRAHAAEMWTANTAEFEKTR--LSVEIYDKFORATSV--- 346
Db 316 SMIGDMIRVLSKRTKEVGEIKAHAAEMKANTAEFRTRF--LSVEIHDKLQRAATIRSM 375
QY 347 -KRKLSAELAGNHNOELTPCRRTL 369
Db 376 ERRRLGLDQRAHSLDMLSPKRSV 399

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## RESULT 4

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Q9H591 PRELIMINARY: PRT: 294 AA.
ID 09H591
AC 09H591;
DT 01-MAR-2001 (Tremblrel. 16, Created)

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QY 169 LFGFLLAGVGDLGTFKGIKAVEDTFIKMNSQTKIRIITII--FILEGCVLVALP 226  
 DB 144 FTLLFETAVVQRYVAVTR--RPVLYFHRMGFSKQVAVLHVAVLLGLTVCSCFFETP 199  
 QY 227 AVFEKIEE-GMSALDAIYFVITLTITIGFDYVAG-GSDIEYIDFKPVVWMIIVGLAY 264  
 DB 200 AAFVSELEDDMNFLEFPCFISLTIGLDYVPGEGYNOKFRELYKIGITCYLLGLIA 259  
 QY 285 FAVALSMIDMLRVISK-----KTEEGVEGFRAHAAE 316  
 DB 260 MLVLETFCE-LHELKFRKMFYVKKDKDEQVHME 295

RESULT 7  
 ID 002821 PRELIMINARY: PRT: 259 AA.  
 AC 002821:  
 DT 01-JUL-1997 (TREMBLrel. 04, Created)  
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)  
 DE DOUBLE PORE POTASSIUM CHANNEL RABCKNK1 (FRAGMENT).  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Orlas M., Velazquez H., Tung F., Desir G.V.;  
 RL Submitted (MAY-1997) to the EMBL/Genbank/DBD databases.  
 DR EMBL; AF004695; AAB61602.1;  
 DR InterPro: IPR001622;  
 DR InterPro: IPR001779;  
 DR PRINTS: PRO1333; 2PORECHANNEL.  
 DR PRINTS: PRO1096; TWIK1CHANNEL.  
 FT NON\_TER 1  
 FT NON\_TER 1  
 FT SEQUENCE 259 AA; 29311 MW; 5546A8BD278E79F3 CRC64;

Query Match 16.8%; Score 353.5; DB 6; Length 259;  
 Best Local Similarity 33.1%; Pred. No. 2.7e-18;  
 Matches 78; Conservative 57; Mismatches 94; Indels 7; Gaps 5;  
 QY 51 FLVAV--VLVLIIGAFAFKALEPOEISQRTTIVYIKOTFIAGACVNSTELDIQOIVA 108  
 DB 26 FLVGLVLTLVGAFAVSSVELPYEDILKQELKLRVEHEECLEQOLEFGLRVLE 85  
 QY 109 AINAGIIPLGNSNOVSHMDLSSFFACTVITTTIGFNISPRTEGKIFCIITVALLGIP 168  
 DB 86 ANNYGVSVSNASGN--WNWDFASALFFASTVLTSTGTGHTVPLSDVGAFCITIVYIGIP 144  
 QY 169 LFGFLLAGVGDLGTFKGIKAVEDTFIKMNSQTKIRIITIIIFLFGCVLVALP 228  
 DB 145 FTLLFETAVVQRYVAVTR--RPVLYFHRMGFSKQVAVLHVAVLLGLTVCSCFFETP 202  
 QY 229 IFKHIE-GMSALDAIYFVITLTITIGFDYVAG-GSDIEYIDFKPVVWMIIVGL 282  
 DB 203 VFSVLEDDMNFLEFPCFISLTIGLDYVPGEGYNOKFRELYKIGITCYLLGL 258

RESULT 8  
 ID 09HBC8 PRELIMINARY: PRT: 330 AA.  
 AC 09HBC8:  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DE TWO PORE POTASSIUM CHANNEL KTS.3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Vega-Saenz de Miera E.C., Lau D.H.P., Zhadina V., Pountney D.,  
 RA Coetzee W., Rudy B.;  
 RT "KTS.2 and KTS.3 Two Novel Human Two Pore K+ Channels Closely Related  
 RT to TASK1".  
 RL Submitted (APR-2000) to the EMBL/Genbank/DBD databases.  
 DR EMBL; AF257081; AAG3127.1;  
 KW Ionic channel.  
 SO SEQUENCE 330 AA; 36130 MW; AA2A54D0615BC5 CRC64;

Query Match 16.8%; Score 351.5; DB 11; Length 330;  
 Best Local Similarity 35.0%; Pred. No. 5.2e-18;  
 Matches 91; Conservative 44; Mismatches 11; Indels 31; Gaps 8;  
 QY 50 IFVAVLYLIIIGAFAFKALEPOEISQRTTIVYIKOTFIAGACVNSTELDIQOIVA 109  
 DB 11 LVLCITCYLLVGAFAVDALAESEAE-SGRORLVQKRGALKEGFAEDYRELERLALQA 69  
 QY 110 --INAGIIPLGNSNOVSHMDLSSFFACTVITTTIGFNISPRTEGKIFCIITVALLGI 167  
 DB 70 EPRRAG-----RQKPFSGYFAITVITTTIGYVAPGTDSGKVFYLLGI 118  
 QY 168 PLFGFLLAGVGDLGTFKGIKAVEDTFIKMNSQTKIRIITIIIFLFGCVLVALP 226  
 DB 119 PLTVTFQSLGERLNAVVRLLAAKCCGLRWTGVSTE--NLVAVGLACATLALG 174  
 QY 227 AVFEKIEE-GMSALDAIYFVITLTITIGFDYVAGSDIFPYKRVWF--WIIVGLA 283  
 DB 175 AAFSHFEGMTFFHAYYCFITLTIGFDVVALQSG--RKLPYVAFSFLYLLGLT 233  
 QY 284 YFAVLSMT-----GDM 295  
 DB 234 VIGAFINLVYRLVVASDM 253

RESULT 9  
 ID 09JL58 PRELIMINARY: PRT: 365 AA.  
 AC 09JL58:  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DE POTASSIUM CHANNEL TASK3.  
 GN KCNK9.  
 OS Cavia porcellus (Guinea pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Hystriocognathi; Caviidae; Cavia.  
 OX NCBI\_TaxID=10141;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=BRAIN;  
 RX MEDLINE=20287530; PubMed=10747866;  
 RA Rajan S., Wismeyer E., Liu G.X., Preisig-Meyer R., Deut J.,  
 RA Karschin A., Derst C.;  
 RT "TASK-3, a novel tandem pore domain acid-sensitive K+ channel. An  
 RT extracellular histidine as pH sensor".  
 RL J. Biol. Chem. 275:16650-16657(2000).  
 DR EMBL; AF212827; AAF63706.1;  
 DR InterPro: IPR000099;  
 DR InterPro: IPR001622;  
 DR InterPro: IPR003092;  
 DR InterPro: IPR003280;  
 DR Pfam; PF02034; TWIK\_channel.1.  
 DR PRINTS: PRO1333; 2PORECHANNEL.  
 DR PRINTS: PRO1095; TASKCHANNEL.  
 SO SEQUENCE 365 AA; 40769 MW; 261DC973FE53AF91 CRC64;

Query Match 16.8%; Score 351.5; DB 11; Length 365;  
 Best Local Similarity 30.1%; Pred. No. 5.9e-18;  
 Matches 94; Conservative 59; Mismatches 110; Indels 49; Gaps 9;

```

OY 42 MKKTVSTIFLV--VLYLTIGAAVFKALBOPQEIISORTTIVIOKQFIACHACVNSTEL 99
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 1 MKKNVRLSLIACFTFYLLVGAAVFDALBESDHREKEELKAEIRIRCKYNI--STED 58
OY 100 DELIOQIVAAI---NAGIIPLGSSNOVSHMDLSSFFPAFTVITTTIGFNGISPRTEGK 156
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 59 YRQLELVISEPHRAGV-----QMKFAGSFFFAITVITTTIGYGAHAPGTDGK 107
OY 157 IECIIYALGIPILGFLAGVGDOLGTIFGKIAKVEDTFIKM-----NVSQTKIR 207
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 108 AFCEFYAVLGIPLTVLMFQSIGERM-----NTPRYLLKRIKCCGKARNTEVS 155
OY 208 IISTIFLFCGVLFVALPAVIFKHIEGWSALDAIYFVITLTITIGEDYVAGSD--IE 265
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 156 MENNVTVGFSCMGTLICGAAGAFSCCEMSFFHAYVYCFITLTITIGEDYVALQSKALQ 215
OY 266 YLDYKPKVWMIIVGLAFPAVLSMIGDMLRVISKKEVGEFRHAA-----EWTA 319
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 216 RKPFYVAFSEFYMLIVGLVIGAFNLV--VLRFLTMNSDERGEGEGALPMPSSVYT 273
OY 320 NVTAPEKTRRR 331
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 274 HISEARQVRR 285

```

## RESULT 10

O90X34

PRELIMINARY: PRT: 299 AA.

```

AC O90X34;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE PUTATIVE POTASSIUM CHANNEL DP4 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Gan L., Joiner W.J., Quinn A.M., Wang L.-Y., Hughes T.,
RA Kaczmarek L.K., to the EMBL/GenBank/DBJ databases.
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF022821; AAD09338.1;
DR InterPro: IPR000099;
DR InterPro: IPR001622;
DR InterPro: IPR003092;
DR InterPro: IPR003280;
DR Pfam: PF02034; TWIK_channel; 1.
DR PRINTS: PRO1333; 2PORECHANNEL.
DR K10NIC channel.
KM Ionic channel.
FT NON_TER 1
FT TER 299
SQ SEQUENCE 299 AA; 33325 MW; DCD41D8A212939C4 CRC64;

```

Query Match 16.5%; Score 344; DB 11; Length 299;

Best Local Similarity 30.7%; Pred. No. 1.6e-17;

Matches 90; Conservative 61; Mismatches 96; Indels 46; Gaps 10;

```

OY 45 KTVSTIFLV--VLYLTIGAAVFKALBOPQEIISORTTIVIOKQFIACHACVNSTELD-E 101
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 2 ENVETLALIVCTFTYLLVGAAVFDALBESDHREKEELKAEIRIRCKYNI--NISEGYE 58
OY 102 LIQIVAAI---NAGIIPLGSSNOVSHMDLSSFFPAFTVITTTIGFNGISPRTEGKIF 158
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 59 ELERVVRLKPKHAGV-----QMRPAGSFFFAITVITTTIGYGAHAPSTDGKGVF 107
OY 159 CIITALLGIPILGFLAGVGDOLGTIFGKIAKVEDTFIKKNVSQTK-----IRII 209
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 108 CMFTALLGIPILTVLMFQSIGERT-----NTPRYLLKRIKCCGKARNTEVSMA 155

```

```

OY 210 STIIFLFCGVLFVALPAVIFKHIEGWSALDAIYFVITLTITIGEDYVAGSD--IEYL 267
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 156 NMVLIFGVSCISTICIGAAAFSYERWTFQAYVYCFITLTITIGEDYVALQKDALQ 215
OY 268 DEYKPKVWMIIVGLAFPAVLSMIGDMLRVISKKEVGEFRHAA-----EWTA 320
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 216 PQYVAFSEFYMLIVGLVIGAFNLV--VLRFLTMNSDERGEGEGALPMPSSVYT 265

```

## RESULT 11

O9H427

PRELIMINARY: PRT: 330 AA.

```

AC O9H427;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE D781B1.1 (A NOVEL PROTEIN SIMILAR TO THE A. CENSITIVE POTASSIUM
DE CHANNEL PROTEIN TASK (KCNK3)).
GN D781B1.1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lovell J.
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL118522; CAC14068.1;
SQ SEQUENCE 330 AA; 36222 MW; 24F428721A1C7 CRC64;

```

Query Match 16.4%; Score 343.5; DB 11; Length 330;

Best Local Similarity 34.6%; Pred. No. 2e-17;

Matches 90; Conservative 44; Mismatches 46; Indels 31; Gaps 8;

```

OY 50 IFLVVLYLTIGAAVFKALBOPQEIISORTTIVIOKQFIACHACVNSTELDIOQIVAA 109
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 11 LVLTCTLYLVGAAVFDALBESDHREKEELKAEIRIRCKYNI--STED 58
OY 110 -INAGIIPLGSSNOVSHMDLSSFFPAFTVITTTIGFNGISPRTEGKIFCIYALGI 167
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 70 EPHRAG-----RQMKFPGSFFFAITVITTTIGYGAHAPSTDGKGVF 107
OY 168 PLFGFLAGVGDOLGTIFGKIAKVEDTFIKKNVSQTK-----IRII 209
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 119 PLTVTFQSGIERLANAVYRLLAKCGLRMTCVS-----NLVYGLACATLALG 174
OY 227 AVTFKHIEGWSALDAIYFVITLTITIGEDYVAGSD-----WILVGLA 283
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 175 AVAFSHEGWTFFHAYVYCFITLTITIGEDYVALQSKALQ-----EWTA 319
OY 284 YFAAVLSMI-----GDW 295
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 234 VIGAFNLVLRFLVAGADW 253

```

## RESULT 12

O76795

PRELIMINARY: PRT: 329 AA.

```

AC O76795;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE PUTATIVE POTASSIUM CHANNEL SUBUNIT N2P38.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditiida; Rhabditiidae;
OC Rhabditiidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Wang Z.-W., Salkoff L.
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.

```









GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 28, 2001, 17:05:47 ; Search time 47.95 Seconds

(Without alignments)  
498.141 Million cell updates/sec

Title: US-09-503-089A-5

Perfect score: 2042  
Sequence: 1 MKRQNVRLALIVCTFTYLL.....STGLHSLSTFFGLMKRRSSV 394

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

A\_Geneseq\_0601:\*

1: /SID58/gcgdata/geneseq/geneseqp/AA1980.DAT:\*

2: /SID58/gcgdata/geneseq/geneseqp/AA1981.DAT:\*

3: /SID58/gcgdata/geneseq/geneseqp/AA1982.DAT:\*

4: /SID58/gcgdata/geneseq/geneseqp/AA1983.DAT:\*

5: /SID58/gcgdata/geneseq/geneseqp/AA1984.DAT:\*

6: /SID58/gcgdata/geneseq/geneseqp/AA1985.DAT:\*

7: /SID58/gcgdata/geneseq/geneseqp/AA1986.DAT:\*

8: /SID58/gcgdata/geneseq/geneseqp/AA1987.DAT:\*

9: /SID58/gcgdata/geneseq/geneseqp/AA1988.DAT:\*

10: /SID58/gcgdata/geneseq/geneseqp/AA1989.DAT:\*

11: /SID58/gcgdata/geneseq/geneseqp/AA1990.DAT:\*

12: /SID58/gcgdata/geneseq/geneseqp/AA1991.DAT:\*

13: /SID58/gcgdata/geneseq/geneseqp/AA1992.DAT:\*

14: /SID58/gcgdata/geneseq/geneseqp/AA1993.DAT:\*

15: /SID58/gcgdata/geneseq/geneseqp/AA1994.DAT:\*

16: /SID58/gcgdata/geneseq/geneseqp/AA1995.DAT:\*

17: /SID58/gcgdata/geneseq/geneseqp/AA1996.DAT:\*

18: /SID58/gcgdata/geneseq/geneseqp/AA1997.DAT:\*

19: /SID58/gcgdata/geneseq/geneseqp/AA1998.DAT:\*

20: /SID58/gcgdata/geneseq/geneseqp/AA1999.DAT:\*

21: /SID58/gcgdata/geneseq/geneseqp/AA2000.DAT:\*

22: /SID58/gcgdata/geneseq/geneseqp/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2042	100.0	394	21	AAV79674
2	2042	100.0	394	21	AAV87291
3	1819	89.1	405	21	AAV95230
4	1116	54.7	374	21	AAV18807
5	1116	54.7	374	21	AAV18813
6	773	37.9	408	22	AAV31804
7	379	18.6	361	22	AAV31805
8	369	18.1	370	20	AAV30648
9	369	18.1	411	20	AAV28497
10	363	17.8	411	20	AAV34133
11	363	17.8	411	20	AAV28496

12	363	17.8	411	22	AAV50044
13	329.5	16.1	393	21	AAV94425
14	329.5	16.1	393	21	AAV94426
15	326.5	16.0	398	20	AAV30647
16	320.5	15.7	336	18	AAV23397
17	320.5	15.7	336	21	AAV79673
18	319	15.6	499	21	AAV90356
19	319	15.6	499	21	AAV79675
20	319	15.6	499	21	AAV94875
21	295.5	14.5	313	20	AAV34132
22	295.5	14.5	313	20	AAV25116
23	295.5	14.5	313	21	AAV90355
24	295.5	14.5	313	21	AAV68737
25	295.5	14.5	313	21	AAV68738
26	294.5	14.4	332	21	AAV90354
27	278.5	13.6	995	22	AAV31799
28	253	12.4	336	17	AAV97986
29	245.5	12.0	395	22	AAV31801
30	231.5	11.3	618	17	AAV79984
31	212.5	10.4	730	22	AAV31800
32	190.5	9.3	383	21	AAV79677
33	176.5	8.6	107	20	AAV28498
34	156.5	7.7	1153	22	AAV31802
35	156	7.6	347	21	AAV79676
36	151	7.4	316	21	AAV14160
37	151	7.4	316	21	AAV40370
38	151	7.4	408	21	AAV41459
39	151	7.4	408	21	AAV40369
40	147.5	7.2	132	22	AAV31803
41	141	6.9	128	21	AAV40248
42	141	6.9	399	21	AAV41831
43	141	6.9	424	21	AAV41830
44	141	6.9	436	21	AAV41829
45	131.5	6.4	646	20	AAV34123

#### ALIGNMENTS

RESULT 1	AAV79674
ID	AAV79674 standard; Protein: 394 AA.
XX	
AC	AAV79674:
XX	
DT	29-AUG-2000 (first entry)
XX	
DE	Human potassium channel TASK1.
XX	
KW	TASK1; TWIK-related acid-sensitive K+ chan
KW	potassium channel; drug screening; hyperten
KW	hypotensive; epilepsy; arrhythmia; vascular
KW	neurodegenerative disease; ischemia; anoxia;
KW	muscle disease; therapy.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	Modified-site
FT	/note= "N-glycosylated"
FT	Modified-site
FT	/note= "O-phosphorylated"
FT	Modified-site
FT	/note= "O-phosphorylated"
FT	Modified-site
FT	/note= "O-phosphorylated"
FT	Modified-site
FT	/note= "O-phosphorylated"
XX	
PM	WO200027871-A2.
XX	
PD	18-MAY-2000.
XX	

Human TREK. Homo  
Human h-TREK poly  
Human h-TREK poly  
A mechanically sen  
TWIK-1 potassium c  
Human potassium ch  
Human TWIK-2 prote  
Human potassium ch  
Human protein clon  
Human potassium ch  
Human hTREK-1 prot  
Human TWIK-4 prote  
K14, a TWIK family  
RT5, a TWIK family  
Human TWIK-3 prote  
Amino acid sequenc  
F22b7.7 potassium  
Amino acid sequenc  
DMOR1 potassium c  
Amino acid sequenc  
Caenorhabditis ele  
Partial h-TREK1 po  
Amino acid sequenc  
Caenorhabditis ele  
Arabidopsis thalia  
Arabidopsis thalia  
Arabidopsis thalia  
Amino acid sequenc  
Human ORFX ORF12 p  
Arabidopsis thalia  
Arabidopsis thalia  
Arabidopsis thalia  
Arabidopsis thalia  
Human potassium ch

PF 09-NOV-1999; 99MO-IB01886.  
 XX  
 PR 09-NOV-1998; 98US-0107692.  
 PR 08-NOV-1999; 99US-0436265.  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 PI Duprat F, Lesage F, Lazdunski M;  
 XX WPI: 2000-376487/32.  
 DR N-PSDB; AAA27746.  
 XX  
 PT New nucleic acid encoding a non-inactivating outwardly rectifying  
 PT potassium transport channel, designated TASK2, useful in the treatment  
 of hypertension or dysfunctions of the kidney, liver or pancreas -  
 XX  
 PS Disclosure; Fig 8; 91pp; English.  
 XX  
 CC The present sequence is that of human TASK1 (TWIK-related  
 CC acid-sensitive K<sup>+</sup> channel), a member of a new family of 2P  
 CC domain potassium channels, also including TWIK-1 (see AAY79673) and  
 CC novel TASK2 (see AAY79675). TASK1 is expressed in many different  
 CC tissues, and at particularly high levels in pancreas and placenta.  
 CC Host cells expressing TWIK-1 family members can be used to screen  
 CC for substances that modulate the activity of members of the TWIK-1  
 CC family of potassium channels. The drugs identified may be  
 CC useful in the treatment of diseases of the heart or of the nervous  
 CC system, such as epilepsy, arrhythmia, vascular diseases,  
 CC neurodegenerative diseases, kidney, liver or pancreas diseases,  
 CC hypertension, diseases associated with ischaemia or anoxia,  
 CC endocrine diseases associated with anomalies of hormone secretion,  
 CC and muscle diseases.  
 CC  
 XX  
 SO Sequence 394 AA:

Query Match 100.0%; Score 2042; DB 21; Length 394;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-214;  
 Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKRQNVFTALIVCTFTYLLVGAANFPALESEPELLERORLEKQELRARIINISGGYE 60  
 DB 1 MKRQNVFTALIVCTFTYLLVGAANFPALESEPELLERORLEKQELRARIINISGGYE 60  
 QY 61 ELERVLRLPHKAGVOMRFAAGSEYFAITVTITGYHAAPSTDGKVFQCFYALLGIP 120  
 DB 61 ELERVLRLPHKAGVOMRFAAGSEYFAITVTITGYHAAPSTDGKVFQCFYALLGIP 120  
 QY 121 TLVWFOGLERINTLVYLLHRAKKGIGMRADYSMANMVLIGFSCISTLCIGAAAFSH 180  
 DB 121 TLVWFOGLERINTLVYLLHRAKKGIGMRADYSMANMVLIGFSCISTLCIGAAAFSH 180  
 QY 181 YEHPFOAYVYCFITLTITGFGDYVALOKDOLQNOPOVAASEFYVILITGITVIGAF 240  
 DB 181 YEHPFOAYVYCFITLTITGFGDYVALOKDOLQNOPOVAASEFYVILITGITVIGAF 240  
 QY 241 LVVLFETMAEDERKDAERHALLTRNGOAGGGGSAHTTDDPAASSTAAGGGGFNNV 300  
 DB 241 LVVLFETMAEDERKDAERHALLTRNGOAGGGGSAHTTDDPAASSTAAGGGGFNNV 300  
 QY 301 AEVLHFOGSCMLWYKREKLQVSIPIWITPRDUSTSPTCVQSHSSPGGGGRVSDPSSR 360  
 DB 301 AEVLHFOGSCMLWYKREKLQVSIPIWITPRDUSTSPTCVQSHSSPGGGGRVSDPSSR 360  
 QY 361 CLCGAPRSALISSVSTGLSLSTFRGIMKRSSV 394  
 DB 361 CLCGAPRSALISSVSTGLSLSTFRGIMKRSSV 394

RESULT 2  
 ID AAY87291  
 XX AAY87291 standard; Protein: 394 AA.

AC AAY87291;  
 XX  
 XX 11-MAY-2000 (first entry)  
 DE Human signal peptide containing protein HSP1-6; SEQ ID NO:68.  
 KW Human: signal peptide containing protein; HSP1-6; diagnosis; cancer;  
 KW inflammation; cardiovascular disease; antic; anti-inflammatory;  
 KW antimicrobial; neuroprotective; anti; anti-inflammatory; hepatotropic;  
 KW antistimulant; gene therapy; cell proliferation; neurological disorder;  
 KW reproductive disorder; developmental disorder; arteriosclerosis;  
 KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;  
 KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;  
 KW Parkinson's disease; Huntington's disease; ovulatory defect;  
 KW muscular dystrophy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200000610-A2.  
 XX  
 PD 06-JAN-2000.  
 XX  
 PF 25-JUN-1999; 99MO-US14484.  
 XX  
 XX 26-JUN-1998; 98US-0090762.  
 PR 31-JUL-1998; 98US-0094983.  
 PR 01-OCT-1998; 98US-0102686.  
 PR 11-DEC-1998; 98US-0112129.  
 XX  
 PA (INCY-) INCYTE PHARM INC.  
 PI Lal P, Tang YT, Gorgone GA, Corley NC, Guebler KJ, Baughn MR;  
 PI Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;  
 PI Bandman O;  
 XX  
 DR WPI: 2000-160673/14.  
 DR N-PSDB; AA298176.  
 XX  
 PT New human signal peptide-containing proteins useful in treatment,  
 PT prevention and diagnosis of e.g. cancer, inflammation and  
 PT cardiovascular disease -  
 XX  
 PS Claim 1; Page 207-208; 327pp; English.  
 XX  
 CC AA298109 to AA298242 encode AAY87224 to AAY87377 which represent the  
 CC human signal peptide-containing proteins HSP1-6 to HSP1-134. HSPs have  
 CC anticancer, anti-inflammatory, antimicrobial, corticotropic, hepatotropic,  
 CC neuroprotective, cardiovascular and antistimulant activities, and can  
 CC be used in gene therapy. HSPs can be used to treat or prevent disorders  
 CC associated with decreased activity or function of HSP. Antagonists of  
 CC HSP are used to treat or prevent disorders associated with increased  
 CC activity or function of HSP. Such diseases include cell proliferation  
 CC (including cancer), inflammation, cardiovascular, neurological,  
 CC reproductive or developmental disorders, (e.g. arteriosclerosis,  
 CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,  
 CC asthma, Crohn's disease, microbial or other infections, congestive or  
 CC ischemic heart disease, Alzheimer's, Parkinson's or Huntington's  
 CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSP  
 CC nucleic acids can be used for the recombinant production of HSP, for  
 CC detecting HSP in standard hybridisation and amplification assays (for  
 CC diagnosis and monitoring), in gene therapy, as antisense,  
 CC triplex-forming or ribozyme therapeutics, for detecting related sequences  
 CC or genetic variations, and for chromosomal mapping. HSP are also used to  
 CC raise specific antibodies (Ab) and to screen for agonists and  
 CC antagonists (potential therapeutic agents). They are used to diagnose, or  
 CC monitor, HSP-related diseases (in usual immunoassays), as therapeutic  
 CC antagonists, in competitive drug screens, and for purification of HSP  
 CC from natural sources.  
 XX  
 SO Sequence 394 AA:

Query Match 100.0%; Score 2042; DB 21; Length 394;

Best Local Similarity 100.0%; Pred. NO. 4.2e-214;  
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MKRONVETLIVCTPFYLLVGVAAFPALISEPELLEROLETEIROELRARVYNLSOGGE	60
Db	1	mkrgnvtlialivctfyllvgaavfalesepellerqrltelrqgellarynlsqgye	60
Qy	61	ELERVVLRLRPHKAGVOMREFAGSEFYAIVITTTIGYHAAPSTDGGVFCMCFALLGIPL	120
Db	61	elervvirlrpkhgvowrffagsfyfalvtlttigyhaapstdggyvfcmfyallyipl	120
Qy	121	TLVWFQSLGERINTLVVYLLHRAKKGIGMRADVSNANMYLIGFSCISITMLCIGAAAFSH	180
Db	121	tlvmfqlsigerintlvyllylhrakkqigmradvsmannmyliffscistlcigaaafsh	180
Qy	181	YEHHTFQAYVYCCITLTJTIGFGBGVYALOKDOLQNOPVVAASFYITLGLVIVAGFLN	240
Db	181	yehhtffqayyccitlttjtgfgbgyvalokdolqnopvvaasfyitlglvivafln	240
Qy	241	LVLVLFRTMAADEKRDAEHRALLTRNGAGCGGGCGGSAHTTPTASTTAAAGGGGFENVY	300
Db	241	lvvlrftmaadeekrdaehrralltrngagggggsgsahtttdasttaaggggfenvy	300
Qy	301	AEVLIHFQSMQSCLMYKSRREKLQISIPMIPRDLSTDTCEQSHSFGGCGRRSDPFSRR	360
Db	301	aevlihfsmqscclmyksrreklqysipmiprdlstdtceqshsp99grrysdpfsrr	360
Qy	361	CICGAPRARSATSSVTGLSLSTFGRGLMKRRSSV	394
Db	361	cicggaprarsatssvtglshlstfgrglmkrrssv	394

XX	RESULT	3
XX	AAV95230	
ID	AAV95230	standard; Protein; 405 AA.
XX	AC	
XX	AAV95230;	
DT	29-AUG-2000	(first entry)
DE	Mouse potassium channel TASK.	
XX	TASK; TWIK-related acid-sensitive K+ channel; mouse;	
KW	potassium channel; drug screening; hypertension;	
KW	hypotensive; epilepsy; arrhythmia; vascular diseases;	
KW	neurodegenerative disease; ischaemia; anoxia; endocrine disease;	
KW	muscle disease; therapy.	
XX		
OS	Mus musculus.	
XX		
XX	Key	Location/Qualifiers
FH	Modified-site	50
FT		/note= "N-glycosylated"
FT	Modified-site	334
FT		/note= "O-phosphorylated"
FT	Modified-site	403
FT		/note= "O-phosphorylated"
FT	Modified-site	404
FT		/note= "O-phosphorylated"
XX		
PN	WO200027871-A2.	
XX		
DD	18-MAY-2000.	
XX		
PF	09-NOV-1999;	99WO-1B01886.
XX		
XX	09-NOV-1998;	98US-0107692.
PR	08-NOV-1999;	99US-0436265.
XX		
XX		
PA	(CNRS ) CNRS CENT NAT RECH SCI.	
XX		
PI	Duprat F, Lesage F, Lazdunski M;	
XX		

DR New nucleic acid encoding a non-inactivating, outwardly rectifying  
XX potassium transport channel, designated TASK-1, useful in the treatment  
PT of hypertension or dysfunctions of the kidney, liver or pancreas -  
XX  
PS Disclosure; Fig 8; 9ipp; English.

CC The present sequence is that of murine TASK<sub>1</sub>, a TASK-related  
CC acid-sensitive K<sup>+</sup> channel), a member of a new family of 2P  
CC domain potassium channels, also including human TASK-1 (see  
CC AAY79673), human TASK1 (see AAY79674) and novel human TASK2 (see  
CC AAY79675). Human and mouse TASK proteins share 85% identity,  
CC indicating that they are products of orthologous genes. Most  
CC cells expressing TASK-1 family members can be used to screen  
CC for substances that modulate the activity of members of the TASK-1  
CC family of potassium channels. The drugs identified may be  
CC useful in the treatment of diseases of the nervous system, or of the nervous  
CC system, such as epilepsy, arrhythmia, vascular diseases,  
CC neurodegenerative diseases, kidney, liver and endocrine diseases,  
CC hypertension, diseases associated with ischemia or anoxia,  
CC hyperthermia, diseases associated with anomalies of hormone secretion,  
CC and muscle diseases.

Query Match	89.1%	Score 1819	Df	Length 405
Best Local Similarity	88.1%	Pred. No. 9.3e		
Matches 357; Conservative	9	Mismatches	Indels 14	Gaps 2

```

QY 4 QMRTTLLIVCTFFYLLVGAVPDALESEPELLERQIL ..QDELRYNVLSSGGYEEL 63
Db 1 envrtllavctffyllvgaavdalesepemtergrtle ..rlhetrarnylssgyeete 60
QY 64 RVVLRRLKPKHAGVOMRPAFGSPFYEAIVITITIGYGHAAPISTPGKVFQCMFYALLGIPLTIV 123
Db 61 rvvrlrlpkhagvqrwfagsfyfaleivittitigyhaaps ..qgkvfcmfyallgipiltll 120
QY 124 MFGSLGRIMTWLVRYLLIHRAKKKGIGMRADVSNANWVL ..LSISTLCIGAAFSHYEH 183
Db 121 mfgslgrintlvryllhrrkrgigmhaevsnaenwvl ..lqavscsltlcigaaafsyer 180
QY 184 WTFQAVYVCFTITTTIGFSDYVALOKDQALQOPQVVA ..VYVITLGLTVICAFNLV 243
Db 181 wtfqavycfittitigfsgdyvalqkdqalqcgpyv ..vyltltgltvicafnlv 240
QY 244 LRFWTNAEDEKRDAAERALLTRNGOAGGGG----- ..AHTTDTASTAAA----- 291
Db 241 lrftwnaedekrdaerallthngvgvlgyslclsg ..lrtpdrvccaagaagvgy 300
QY 292 --GGGGRNNVYAENVLFHOSMCSLMWSRKLQYSTIM ..DLSTSDTCVEDSHSSPG 349
Db 301 gvvgsgfrnyaevlthqsmcscfwmysreklqysipm ..dlstsdctevhshsspg 350
QY 350 GGRSDTPSRRCICSGAPRAAISVSNGLSLSPRGLV ..SSV 394
Db 361 ggrsdtpsrncicsgpraisvsnglnslaafrlv ..ssv 405

```

	RESULT	4
AAAB18807	ID	AAAB18807 standard; Protein; 374 AA.
XX	AC	
XX	AAAB18807;	
XX	DT	22-JAN-2001 (first entry)
DE		Amino acid sequence of a human DKCN1 polypeptide.
XX		
XX		
KW		Human; DKCN1; potassium channel; cancer; psychiatric disorder; schizophrenia; neuro-
KM		cardiovascular disease; inflammatory diseas-
KW		psychiatric disorder; schizophrenia; neuro-
KM		cardiovascular disease; inflammation; pain; depressive disease;



QY 181 YEHWFQAYVYCFITLTITGFGDYVALOKDQLOTPQVAFSVYITLGLVIGAFIN 240  
 DB 181 ceewstfthayyciflittltitgdyvalqkpklyvatsfmyllvgtlvigafin 240  
 QY 241 LVVLRFTMAAEDEKRDARALTRNGAGGGGCGGSAHTTPTASTAAGGGGFENY 300  
 DB 241 lvvlrftmasederrdaerasl-----agrrnsmvlihepepps-----rpy 286  
 QY 301 -AEVLHFQSMCGLWYKSRKQLQYIPMIIPRLSTSDTCVEOSHSSPGGGRYSDTPSR 359  
 DB 287 kadvpdlqswcscctcyrsq---ygrsvapqnsfsaklaphyfnhsykieeispstlk 343  
 QY 360 RCLCAGAPRAISVSSTGLHSLSTFRLGKMRSSV 394  
 DB 344 nsilfp---spissispgjhsfchqrlmkrrksv 374

RESULT 6  
 AAB31804 ID AAB31804 standard; Protein; 408 AA.  
 AC AAB31804;  
 XX 15-MAY-2001 (first entry)  
 DT Amino acid sequence of a TWIK7 polypeptide.  
 DE  
 XX Tandem pore domain weak inward potassium protein: TWIK; TWIK2; TWIK3;  
 KM TWIK4; TWIK5; TWIK6; TWIK7; TWIK1; pesticide; ion channel.  
 XX Drosophila melanogaster.  
 OS  
 FH Key Location/Qualifiers  
 FT Domain 9..25  
 FT Domain /note= "transmembrane domain 1"  
 FT Domain 78..101  
 FT Domain /note= "Pore domain"  
 FT Domain 109..125  
 FT Domain /note= "transmembrane domain 2"  
 FT Domain 161..177  
 FT Domain /note= "transmembrane domain 3"  
 FT Domain 184..207  
 FT Domain /note= "pore domain"  
 FT Domain 224..240  
 FT Domain /note= "transmembrane domain 4"  
 XX  
 PN MO200109301-A2.  
 PD 08-FEB-2001.  
 XX 27-JUL-2000; 2000MO-US20439.  
 PF 28-JUL-1999; 99US-0362842.  
 PR  
 XX (GENO-) GENOPTERA LLC.  
 PA Francis-Lang HL, Gillett LA, Margolis JS, Reddy BP, Winslow JM;  
 PI Luo Y, Gendreau SB, Jacobus DA, Tietjen K, Nauen R, Jeschke P;  
 XX WPI; 2001-159864/16.  
 DR N-PSDB; AAF25380.  
 XX  
 XX New tandem pore domain weak inward rectifying potassium ion (TWIK)  
 PT channel nucleic acids and proteins, useful in assays for identifying  
 PT candidate compounds which are potential pesticides or therapeutics -  
 XX  
 PS Claim 5; Page 83-85; 96pp; English.  
 XX  
 CC The present sequence represents tandem pore domain weak inward potassium  
 CC (K+) (TWIK) polypeptide. The specification describes TWIK2, TWIK3, TWIK4,  
 CC TWIK5, TWIK6, TWIK7, and TWIK1. The TWIK channel nucleic acids and  
 CC proteins are used in screening assays to identify candidate compounds  
 CC which are potential pesticides or therapeutics. The TWIK channel nucleic

CC acids can be used for generating mutant phages in animal models or  
 CC in living cells that can be used to study ion channels, their  
 CC regulation, and their use as pesticide or ion primers. TWIK  
 CC hybridisation probes and replication/amplicons are used to screen  
 CC channel proteins are useful as immunogens to create monoclonal or  
 CC polyclonal antibodies, and in assays to identify molecules that would  
 CC specifically bind to them. Genetically engineered metazoan invertebrate  
 CC animals may be used in studying TWIK channels, and for screening  
 CC and identifying new drug targets, therapeutic agents, diagnostics and  
 CC prognosis useful in treating disorders associated with ion channels.  
 XX Sequence 408 AA:

Query Match 37.9%; Score 773; Df 1  
 Best local similarity 43.6%; Pred. No. 1.3  
 Matches 164; Conservative 66; Mismatches 98

QY 1 MKRONVFTALIVCTETYLIVGAAPDALESEPELIEH 306ELRARNVLSGGYE 60  
 DB 1 mkkqnvrtllivctfyllivgaavfdaleselekrrk 3aedmlkkynisqgdfk 60  
 QY 61 ELERVYLRLKPKAGVOMRAGSFYFAITVITTTGVG 10GGRVECFYVALLGIPL 120  
 DB 61 vmetvylkseshkagqwkltgaltgaltvltltgyg 10vgtlftmcyaltgalt 120  
 QY 121 TLVWFOSLGRINTLVYVLLHRAKKGIMRADVSMAK 10FSCISTLCI--GAAP 178  
 DB 121 glvmfsgigervrnllsylvkavrsllrckrtvasew 10vltlssltlaggaaf 178  
 QY 179 SHYEHWFQAYVYCFITLTITGFGDYVALOKDQALC 10A5HYVILUTGLTVIGAF 238  
 DB 179 sklegwysidsvyccflittltitgdyvalqrdnalor 10vttalllllfgaltvaas 238  
 QY 239 LNVVLRFTMAAEDEKRDARALTRNGAGGGGCGGSAHTTPTASTAAGGGGFENY 306ELRARNVLSGGYE 60  
 DB 239 lnlvlrftmasederrdaerasl-----agrrnsmvlihepepps-----rpy 286  
 QY 286 SSTAAAGGGGFRNVYAEVLHFQSMCSC----- 10A5HYVILUTGLTVIGAF 238  
 DB 286 -----nissmschclngnrth 10vttalllllfgaltvaas 238  
 QY 321 -LQYSIPMIIP-RDLS 334  
 DB 339 hirlhlpevymqdl 354

RESULT 7  
 AAB31805 ID AAB31805 standard; Protein; 361 AA.  
 AC AAB31805;  
 XX 15-MAY-2001 (first entry)  
 DT Amino acid sequence of a cpb-TWIK1 polypeptide.  
 DE  
 XX Tandem pore domain weak inward potassium protein: TWIK; TWIK2; TWIK3;  
 KM TWIK4; TWIK5; TWIK6; TWIK7; TWIK1; pesticide; ion channel.  
 XX Leptinotarsa decemlineata.  
 OS  
 FH Key Location/Qualifiers  
 FT Domain 46..60  
 FT Domain /note= "transmembrane domain 1"  
 FT Domain 125..149  
 FT Domain /note= "pore domain"  
 FT Domain 156..176  
 FT Domain /note= "transmembrane domain 2"  
 FT Domain 204..231  
 FT Domain /note= "transmembrane domain 3"  
 FT Domain 235..259  
 FT Domain /note= "pore domain"

FT	Domain	274..296	/note="transmembrane domain 4"
XX			
FN	MO200109301-A2.		
XX			
PD	08-FEB-2001.		
XX			
PF	27-JUL-2000; 2000MO-US20439.		
XX			
PR	28-JUL-1999; 99US-0362842.		
XX			
PA	(GENO-) GENOPTERA LLC.		
XX			
PI	Francis-Dang HL, Gillett LA, Margolis JS, Reddy BP, Winslow JW;		
XX	Luo Y, Gendreau SB, Jacobus DA, Tietjen K, Nauen R, Jeschke P;		
XX	WPI: 2001-159864/16.		
DR	N-PSDB: AAF25381.		
XX			
FT	New tandem pore domain weak inward rectifying potassium ion (TWIK)		
PT	channel nucleic acids and proteins, useful in assays for identifying		
XX	candidate compounds which are potential pesticides or therapeutics -		
XX			
PS	Claim 5; Page 87-88; 96pp: English.		
XX			
CC	The present sequence represents tandem pore domain weak inward potassium		
CC	(K+) (TWIK) polypeptide. The specification describes TWIK2, TWIK3, TWIK4		
CC	TWIK5, TWIK6, TWIK7, and TWIK1. The TWIK channel nucleic acids and		
CC	proteins are used in screening assays to identify candidate compounds		
CC	which are potential pesticides or therapeutics. The TWIK channel nucleic		
CC	acids can be used for generating mutant phenotypes in animal models or		
CC	in living cells that can be used to study the ion channels, their		
CC	regulation, and their use as pesticide or drug targets, and as		
CC	hybridisation probes and replication/amplification primers. TWIK		
CC	channel proteins are useful as immunogens to generate monoclonal or		
CC	polyclonal antibodies, and in assays to identify molecules that would		
CC	specifically bind to them. Genetically engineered metazoan invertebrate		
CC	animals may be used in studying TWIK channel activity, and for screening		
CC	and identifying new drug targets, therapeutic agents, diagnostics and		
CC	prognosis useful in treating disorders associated with ion channels.		
XX			
Sequence	361 AA;		

[illegible]

**RESULT 8**

ID AAY30648 standard; Protein: 370 AA.

XX AC AAY30648;

XX DT 18-NOV-1999 (first entry)

DE A mechanically sensitive potassium channel protein TREK-1.

XX KW Mechanically sensitive potassium channel protein; TREK-1;  
KW polyunsaturated fatty acid; arachidonic acid; riluzole; heart disease;  
KW nervous system disease; epilepsy; cardiovascular disease; arrhythmia;  
KW neurodegeneration; ischemia; anoxia; hormone secretion abnormality;  
KW muscular disease.

OS Mus sp.

XX PN W09945108-A2.

XX PD 10-SEP-1999.

XX PF 23-FEB-1999; 99WO-FR00404.

XX PR 05-MAR-1998; 98FR-0002725.

XX PA (CNRS ) CNRS CENT NAT RECH SCI.

XX PI Honore E, Fink M, Lazdunski M, Lesage F, Durrat F;  
DR WPI: 1999-551038/46.  
DR N-PDSB; AAZ10607.

PT New mechanically sensitive potassium channels used to screen for  
PT specific modulators, potential therapeutic agents for heart and nervous  
PT system disorders -

PX Claim 3; Page 23-25; 40pp; French.

XX The present sequence represents a mechanical sensitive potassium  
XX channel protein designated TREK-1. The protein is activated by  
XX polyunsaturated fatty acids, particularly arachidonic acid, and by  
XX riluzole. The protein is used to screen for specific modulators which  
XX are useful for treating or preventing diseases of the heart and nervous  
XX systems in humans and animals, e.g. epilepsy, cardiovascular disease  
XX (arrhythmia), neurodegeneration (particularly here associated with  
XX ischemia or anoxia), abnormalities of hormone secretion and muscular  
XX disease. The protein itself may be used to detect these diseases.  
CC Antibodies specific for the protein are used to detect it in tissues,  
CC also as therapeutic inhibitors or activators.

SQ Sequence 370 AA;

Query Match 18.1%, Score 369, DB Length 370:  
Best Local Similarity 31.6%, Pred. No. 1.3e+06  
Matches 93; Conservative 57; Mismatches 36; Indels 42; Gaps 9;

OY 1 MKROWRTLALIVCFYLLVGAAAFDALSREPELER...IKROELRARINLSOGCYE 60  
DB 42 mkwkvstiflvv-vylllgaavfaiklegqeqsqqr...ilgqftlaqcavns--t 97  
OY 61 ELERVLRL-KPRKAGV-----QMRPAGSEFVA...TTTIGYGHAAPSTDGKV 108  
DB 98 eldeiqlqvaaiaaagiliplnssngvshwdlgssffic...ltligfgnlsprteggki 157  
OY 109 FCMFYALLGIPLTVLFOSLSGERINTLVRYLLHRAKKG...RAD-----VSM 156  
DB 158 fcilyalligirpfkgllagvgdqdlgtlf-----gkikavedtfikwnvsqtikiri 208  
OY 157 ANMWLIGFSCSTLCIGAAAFSHHEHMTFFOATYYCF...TTICFGDYVALOKKOALOT 216  
DB 209 istliffcglcvfalpaavfkhhagsaldadyfvyv...ctyfgdyvaagsd--ley 266

QY 217 QPOYVAFSEVYILGLTVIGAFNLV--VLEFMTMAEDERD-AEHRALLTRN 267  
 Db 267 ldfykpvrwfwlvglayfaavismigdlrvlskckeevgetrahaewtan 320

## RESULT 9

AAV28497  
 ID AAV28497 standard; Protein; 411 AA.

XX AAV28497;

XX 12-OCT-1999 (first entry)

XX Mouse h-TREK1 polypeptide.

XX h-TREK1: two pore potassium channel; inflammatory disease;  
 XX chromosome 1q32.

XX Mus musculus.

XX MO9937762-A1.

XX 29-JUL-1999.

XX 02-DEC-1998; 98MO-EP07805.

XX 09-OCT-1998; 98GB-0022135.

XX 27-JAN-1998; 98EP-0300570.

XX (SMIK ) SMITHKLINE BEECHAM PLC.

XX Chapman CG, Meadows HJ;

XX WPI: 1999-469126/39.

XX DR N-PSDB; AA200040.

XX New two pore potassium channel used for, e.g. treatment of cancer,  
 XX pulmonary, cardiovascular and inflammatory diseases

XX Claim 3; Page 26; 44pp; English.

XX This sequence is the mouse h-TREK1 polypeptide, encoded by the h-TREK1  
 XX polynucleotide AA200040. h-TREK1 is a two pore potassium channel.

XX The polynucleotide sequence of h-TREK1 can be used to diagnose a  
 XX disease or susceptibility to a disease related to expression or activity

XX of h-TREK1 polypeptides. The methods of diagnosis may be used in the  
 XX treatment of diseases including cancer, pulmonary, cardiovascular, and

XX inflammatory diseases, pain, psychiatric disorders including depression  
 XX and schizophrenia, neurodegenerative diseases including Alzheimer's,  
 XX stroke, and head trauma and neurological disorders including migraine.

XX Sequence 411 AA;

Query Match 18.1%; Score 369; DB 20; Length 411;  
 Best Local Similarity 31.6%; Pred. No. 1.5e-31;

Matches 93; Conservative 57; Mismatches 102; Indels 42; Gaps 9;

QY 1 MKRONVTLLALVCTFFYLLVGAAPDASEPPLRORLENOELRARNYLSGGYE 60  
 Db 42 mkwktvstflfv--vylilgaavfkaleqpgisqrtlviqkqfllaqhaevns--t 97  
 QY 61 ELEENVRL-KPRKAGV-----OMRFAGSFYFATVITTTIGYGAAPSTDGKY 108  
 Db 98 eldeliqvvaalagilipgnssngvshwdlgsstffagvticifgnlsprteggk 157  
 QY 109 FCFMFALGIPDLTLMFQSLGERINTLVRYLLHRAKGLGNRRAD-----VSM 156  
 Db 158 fcllyallgipdlfllagvgdqlgltf-----gkglakvedcfikwnvsqtklri 208  
 QY 157 ANNVLIFFSCISTLTCGAAAFSHYEMWTFQOAYVYCFITLTITGFGDYALAKQALQT 216

Db 209 lsliliflfgcvlvalpavifkhiagsaldalyfv--lfgdyvaggds--ley 266  
 QY 217 QPOYVAFSEVYILGLTVIGAFNLV--VLEFMTMAEDERD-AEHRALLTRN 267  
 Db 267 ldfykpvrwfwlvglayfaavismigdlrvlskckeevgetrahaewtan 320

## RESULT 10

AAV34133  
 ID AAV34133 standard; Protein; 411 AA.

XX AAV34133;

XX 30-NOV-1999 (first entry)

XX Human potassium channel K-Hnov59.

XX Potassium channel; ataxia; arrhythmia; epilepsy; Bartter's syndrome;  
 XX cardiovascular disorder; CNS disorder; renal disorder.

XX Homo sapiens.

XX MO9943696-A1.

XX 02-SEP-1999.

XX 22-FEB-1999; 99MO-US03826.

XX 19-JAN-1999; 99US-0116448.

XX 25-FEB-1998; 98US-0076687.

XX 07-AUG-1998; 98US-0095836.

XX (AXYS-) AXYS PHARM INC.

XX Curran ME, Hu P, Miller AP, Rutter M, et al;

XX WPI: 1999-527591/44.

XX DR N-PSDB; AA211915.

XX New nucleic acids encoding mammalian K-Hnov proteins, useful for the diagnosis and treatment of episodic ataxia  
 XX with myokymia, cardiac arrhythmia, epilepsy, and Bartter's syndrome

XX Claim 3; Page 104-105; 112pp; English.

XX This sequence represents the human K-Hnov59 potassium channel.

XX K-Hnov proteins have a high degree of homology to known potassium  
 XX channels and may be alpha subunits, which form the functional channel,  
 XX or accessory subunits that act to modulate channel activity. K-Hnov59

XX is a 4 transmembrane domain, 2 pore domain potassium channel. The gene  
 XX is located on chromosome 19, determined via chromosome

XX localisation using primers AA211919 and AA211920. K-Hnov cDNAs  
 XX were isolated by extension of expressed sequence tags (ESTs) which were

XX related but not identical to known human potassium channels. Potential  
 XX polymorphisms detected as sequence variants between multiple

XX independent clones. Potassium channels have critical roles in various  
 XX cell types and biochemical pathways. Defective potassium channels are

XX known to cause four human diseases: episodic ataxia with myokymia;  
 XX cardiac arrhythmia (long QT syndrome); epilepsy; and Bartter's syndrome.

XX As potassium channels are critical components of virtually all cells,  
 XX it is likely that abnormal potassium channels are also implicated in

XX certain renal, cardiovascular and central nervous system (CNS)  
 XX disorders. Nucleotides encoding K-Hnov proteins may be used for

XX identifying homologous or related proteins and the DNA sequences encoding  
 XX them. They may be used to produce compositions that modulate the

XX expression and function of the K-Hnov protein and in studying the  
 XX biochemical pathways associated with it. They may also be used for the

XX recombinant production of K-Hnov protein in mammalian cell cultures.  
 XX Additionally, such nucleotides may be used in gene therapy protocols for

XX the treatment of diseases associated with abnormal potassium channels.

XX Sequence 411 AA;

Seq	Sequence	411 AA;	17.88;	Score 363;	DB	Length 411;
Query Match	Best Local Similarity	31.08;	Pred. No. 7e-3			
Matches 91;	Conservative 59;	Mismatches				
1 MKRQNRVRLAIIVTFTFYLLVGAAPDALESEDELLER						
42 mkwvstfliv--vlylllgavlkaleqphelsqr						
61 ELERVRLT-KPKAGV-----QWRFGSFPV						
98 eldelldqivaanagilpigntsengshwdlgsstft						
109 FCMRYALLGIPLTLMVNFQSGERINTLVRYLHRANKG						
158 fcllyallgiprlfplglagvgdqlgrtf-----						
157 ANMYLIGFESCIPTLCIGAAPFSHYEHWPFOAYVYCF						
209 istliffllgcvlvalpalalflkhiegwsaldaiyfv						
217 QPQYVAESFYIILGTLTGATGATNLV--VLRFTMNAE						
267 ldfkpvvfwfmlvglayfaavismigdwlrviskkt						
RESULT 12						
AAB50044	standard; Protein; 411 AA.					
AAB50044;						
19-MAR-2001	(first entry)					
Human TREK.						
Human TREK; 2P domain potassium channel; 1						
neurological excitability; neurotransmitter re-						
attention deficit disorder; sleep-related anxi-						
Parkinson's chorea; Huntington's chorea; ce-						
erecille dysfunction; alopecia.						
Homo sapiens.						
WO200072863-A2.						
07-DEC-2000.						
01-JUN-2000; 2000WO-GB02107.						
01-JUN-1999; 99GB-0012733.						
(SMIK ) SMITHKLINE BEECHAM PLC.						
Hervieu GJ, Meadows HJ, Randall AD;						
WPI; 2001-080422/09.						
N-PSDB; AAC90412.						
Use of human TREK1 polypeptide, polynucleot						
modulators of h-TREK1 polypeptides for treat						
disorders, addiction and dyskinesias includ						
Huntington's chorea						
Claim 7; Page 29; 35pp; English.						
The present sequence is human TREK1 (h-TREK						
2P domain potassium channel family of prote						
control of resting membrane potentiality. Modu						
therefore affect neuronal excitability, th						





XX MPI: 2000-365583/31.  
 DR N-PSDB; AAA27106.  
 XX Novel isolated h-TRAAK polypeptides belonging to the potassium channel  
 PT family of polypeptides, useful for the diagnosis and treatment of  
 PT h-TRAAK related disorders, e.g. depression and schizophrenia -  
 XX  
 PS Claim 12; Pages 21 and 22; 35pp; English.  
 XX  
 CC Functional genomics was used to identify h-TRAAK polypeptides and  
 CC h-TRAAK polynucleotides from human tissue samples. h-TRAAK  
 CC polypeptides have homology to the 2P domain potassium channel family of  
 CC polypeptides. The h-TRAAK polypeptides and polynucleotides may  
 CC be used in diagnostic assays for conditions related to h-TRAAK  
 CC imbalance and for identifying agonists and antagonists of h-TRAAK  
 CC polypeptides. The h-TRAAK polypeptides and polynucleotides may also  
 CC be useful for treatment and prevention (e.g. as vaccines) of certain  
 CC diseases, such as pain, psychiatric disorders including depression and  
 CC schizophrenia, neurodegenerative disease including Alzheimer's, stroke  
 CC and head trauma and neurological disorders including migraine and  
 CC epilepsy. The present sequence is human h-TRAAK protein #2.  
 CC  
 XX  
 SQ Sequence 393 AA;

Query Match 16.1%; Score 329.5; DB 21; Length 393;  
 Best Local Similarity 31.0%; Pred. No. 2.9e-27;

Matches 98; Conservative 43; Mismatches 112; Indels 63; Gaps 8;

OY 9 LALIVCTFTYLLVGAAPDASEPRLIERORLELRODELARVNLNQ----- 56  
 DB 7 Lallalvlllylvgalvfgaleqhegqagrelgevrekltrahpcvsdqlillkeva 66  
 OY 57 ---GVEELERVVLRKPKRAGVOMRPAISFYATVITTTIGGHAAPSTGCKVFCMEY 113  
 DB 67 dalggagpelsstusnsisa---wldgsaifsgfllitllygvaltdagrlfclly 123  
 OY 114 ALLGIPLVLMFOSLGERINTLVRYLLHRAKGLGMRAD-----VSMANVLI 163  
 DB 124 alvgplrlflllagvdrfgsslrh-----gighleaiflkwyppelvrlylsamfl 176  
 OY 164 FESCISTLCIGAAAFSHHEWTFEFOAYVYCFTLTITIGEDVVALQKDALQTOPQYVAR 223  
 DB 177 llgcllfvlrptfvcymedwskleaifvlylcltvgfydgadpr--qdsapyqrl 234  
 OY 224 SFVYITLGT-----LTVIGAFNLVLRMTNADDEKRDARLRLTRNGAGGGGG 276  
 DB 235 vwflllglayfasvltlignwlvrvsr-----traemgltaga 275  
 OY 277 GSAHTTDTASSTAAAG 292  
 DB 276 aswtgvtarvtcrag 291

RESULT 15

AA30647  
 ID AAY30647 standard: Protein; 398 AA.

XX AAY30647;

XX 18-NOV-1999 (first entry)

DE A mechanically sensitive potassium channel protein TRAAK.

XX Mechanically sensitive potassium channel protein; TRAAK;  
 KW polynunsaturated fatty acid; arachidonic acid; riluzole; heart disease;  
 KW nervous system disease; epilepsy; cardiovascular disease; arrhythmia;  
 KW neurodegeneration; ischemia; anoxia; hormone secretion abnormality;  
 KW muscular disease.

XX Mus sp.

PN WO9945108-A2.  
 PD 10-SEP-1999.  
 XX  
 XX 23-FEB-1999; 99WO-FR00404.  
 PF  
 XX 05-MAR-1998; 98FR-0002725.  
 PR  
 XX  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 XX  
 PI Honore E, Fink M, Lazdunski M, Lesage F,  
 DR MPI: 1999-551038/46.  
 DR N-PSDB; AA210606.  
 XX  
 PT New mechanically sensitive potassium channel protein used to screen for  
 PT specific modulators, potential therapeutic drugs for heart and nervous  
 PT system disorders -  
 XX  
 PS Claim 2; Fig 1; 40pp; French.  
 XX  
 CC The present sequence represents a mechanical sensitive potassium  
 CC channel protein designated TRAAK. The protein is activated by  
 CC polynunsaturated fatty acids, particularly a polyunsaturated fatty acid, and by  
 CC riluzole. The protein is used to screen for specific modulators which  
 CC are useful for treating or preventing diseases of the heart and nervous  
 CC systems in humans and animals, e.g. epilepsy, cardiovascular disease  
 CC (arrhythmia), neurodegeneration (particular disease associated with  
 CC ischemia or anoxia), abnormalities of hormone regulation and muscular  
 CC disease. The protein itself may be used to detect it in tissues,  
 CC antibodies specific for the protein are used to detect it in tissues,  
 CC also as therapeutic inhibitors or activators.  
 CC  
 XX  
 SQ Sequence 398 AA;

Query Match 16.0%; Score 326.5; DB 21; Length 398;  
 Best Local Similarity 31.5%; Pred. No. 6.4e-27;

Matches 85; Conservative 45; Mismatches 112; Indels 45; Gaps 7;

OY 9 LALIVCTFTYLLVGAAPDASEPRLIERORLELRODELARVNLNQ----- 56  
 DB 7 Lallalvlllylvgalvfgaleqhegqagrelgevrekltrahpcvsdqlillkeva 66  
 OY 68 RLKRPKAGV-----WRFAGSFYATVITTTIGGHAAPSTGCKVFCMEY 115  
 DB 67 ealggagpelsstusnsisa---wldgsaifsgfllitllygvaltdagrlfclly 126  
 OY 116 LGIPLVLMFOSLGERINTLVRYLLHRAKGLGMRAD-----VSMANVLI 162  
 DB 127 vglplrlflllagvdrfgsslrh-----gighleaiflkwyppelvrlylsamfl 179  
 OY 163 GFESCISTLCIGAAAFSHHEWTFEFOAYVYCFTLTITIGEDVVALQKDALQTOPQYVAR 220  
 DB 180 g---cllfvlrptfvcymedwskleaifvlylcltvgfydgadpr--qdsapyqrl 234  
 OY 221 -----VAFSFVYITLGTITVIGAFNLVLR 245  
 DB 235 lvwflllglayfasvltlignwlvrvsr-----traemgltaga 275

Search completed: August 28, 2001, 17:05:48  
 Job time: 1893 sec



**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 28, 2001, 17:06:22 ; Search time 28.01 Seconds

(without alignments)  
289,632 Million cell updates/sec

Title: US-09-503-089a-5

Perfect score: 2042  
Sequence: 1 MKRQNVRLALIVCTFTYLL.....STGLHSLSTFGLMKRRSSV 394

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Issued\_Patents\_AA:\*  
1: /cgn2\_6/prodata/2/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/prodata/2/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/2/iaa/5A\_COMB.pep:\*  
4: /cgn2\_6/prodata/2/iaa/5B\_COMB.pep:\*  
5: /cgn2\_6/prodata/2/iaa/CCTUS\_COMB.pep:\*  
6: /cgn2\_6/prodata/2/iaa/backfilest1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	369	18.1	411	4	US-09-236-080-6
2	363	17.8	411	4	US-09-236-080-2
3	320.5	15.7	336	3	US-08-749-816-2
4	253	12.4	336	1	US-08-332-312-4
5	231.5	11.3	618	1	US-08-332-312-2
6	190.5	9.3	383	3	US-08-749-816-4
7	176.5	8.6	107	4	US-09-236-080-4
8	156	7.6	347	3	US-08-749-816-3
9	103	5.0	532	1	US-08-288-405A-10
10	102.5	5.0	626	2	US-08-956-242-2
11	102.5	5.0	626	1	US-09-351-215-2
12	99.5	4.9	494	3	US-08-464-340A-4
13	99.5	4.9	494	5	PCT-US94-08449A-4
14	99.5	4.9	888	3	US-08-956-242-4
15	99.5	4.9	888	3	US-09-351-215-4
16	97	4.8	255	2	US-09-342-084-11
17	94	4.6	1159	3	US-08-956-242-13
18	94	4.6	1159	3	US-09-351-215-13
19	94	4.6	1159	4	US-09-226-012-2
20	94	4.6	1159	4	US-09-226-012-4
21	92.5	4.5	233	4	US-09-342-084-12
22	90.5	4.4	407	2	US-08-742-440A-3
23	90.5	4.4	509	2	US-09-031-392-6
24	90.5	4.4	509	2	US-09-299-549-6
25	88	4.3	376	1	US-08-614-801A-6
26	87	4.3	528	2	US-08-527-152-2
27	85	4.2	27	3	US-08-749-816-5

28	85	4.2	27	3	US-08-749-816-6	Sequence 6, Appl
29	84.5	4.1	281	4	US-09-053-702-2	Sequence 2, Appl
30	84	4.1	1239	2	US-08-937-931-2	Sequence 2, Appl
31	84	4.1	1239	4	US-09-285-502-2	Sequence 2, Appl
32	81	4.0	553	3	US-09-083-351-2	Sequence 2, Appl
33	81	4.0	553	4	US-09-083-352-2	Sequence 2, Appl
34	80	3.9	242	2	US-08-553-497A-2	Sequence 26, Appl
35	80	3.9	242	2	US-08-553-497A-2	Sequence 26, Appl
36	80	3.9	244	2	US-08-553-497A-2	Sequence 22, Appl
37	80	3.9	488	1	US-08-115-365-2	Sequence 2, Appl
38	80	3.9	488	1	US-08-586-897-2	Sequence 2, Appl
39	79.5	3.9	270	2	US-08-652-507-2	Sequence 2, Appl
40	79.5	3.9	817	2	US-08-820-170A-2	Sequence 28, Appl
41	79.5	3.9	817	3	US-09-055-699-28	Sequence 28, Appl
42	79.5	3.9	817	4	US-09-273-565-28	Sequence 28, Appl
43	79.5	3.9	829	2	US-08-820-170A-31	Sequence 31, Appl
44	79.5	3.9	829	3	US-09-055-699-31	Sequence 31, Appl
45	79.5	3.9	829	4	US-09-273-565-31	Sequence 31, Appl

#### ALIGNMENTS

RESULT 1  
US-09-236-080-6  
; Sequence 6, Application US/09236080  
; Patent No. 6242217  
; GENERAL INFORMATION:  
; APPLICANT: Helen Meadows  
; APPLICANT: Conrad Chapman  
; TITLE OF INVENTION: No. 6242217e1 Compounds  
; FILE REFERENCE: GP30031  
; CURRENT APPLICATION NUMBER: US/09/236,080  
; CURRENT FILING DATE: 1999-01-25  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FASTSEQ for Windows Version 3.0  
; SEQ ID NO 6  
; LENGTH: 411  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-236-080-6

Query Match	18.1%	Score 369;	DB 4;	Length 411;
Best local Similarity	31.6%	Pred. No. 1.6e-12;		
Matches	93;	Conservative	57;	Mismatches 102; Indels 42; Gaps 9;
OY	1	MKRONVRLALIVCTFTYLLVGAIVDALESEPELLERORL:RODELARYLSGGYE 60		
DB	42	MKRWVSTIFLVV--VLYLIGAIVKALEOPOEISQRTIVIOKOTFLAORACVNS--T 97		
OY	61	ELERVLRL-KPHKAGV-----QWRFAFSFPAIT-ATPGYGAAPSTDGKV 108		
DB	98	ELDELIOQVIAINACIITPLGNSNOVSHMDLGSFFFGVITTTIGFGNISRTGKRI 157		
OY	109	PCMFVALLGIPITLVNFOSLGERINTLVRYLLHRAKGLGMRAD-----VSM 156		
DB	158	FCIIVALLGIPLEGFLAGVDQLGTF-----GCIKAVEDTFTKMNVSQTKIRI 208		
OY	157	ANNVILGFSCISTLCIGAAPSHYEHMTFPQAYYYCFITTTIGGDDVALOKDALOT 216		
DB	209	ISTIIIFLEGCVLFVLPVIFKHIGWSALDAIYFV--FTIGGDDVAGSD--IEY 266		
OY	217	QPOYVAFSEVYITGLTVIGAFNLV--VLRPMTNMI--ID-AEHRALLTRN 267		
DB	267	LDFYKRVWFVILVGLAYFRAVLSMIGDMLRVISKTK--EFAHAAEWTAN 320		
RESULT 2				
	US-09-236-080-2			
	; Sequence 2, Application US/09236080			
	; Patent No. 6242217			
	; GENERAL INFORMATION:			

```

:
: APPLICANT: Helens Meadows
: APPLICANT: Conrad Chapman
: TITLE OF INVENTION: No. 6242217el Compounds
: FILE REFERENCE: 6P30031
: CURRENT APPLICATION NUMBER: US/09/236,080
: CURRENT FILING DATE: 1999-01-25
: NUMBER OF SEQ ID NOS: 6
: SOFTWARE: FastSeq for Windows Version 3.0
:
: SEQ ID NO 2
:
: LENGTH: 411
:
: TYPE: prt
:
: ORGANISM: Homo sapiens
:
US-09-236-080-2

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Query Match	17.8%;	Score 363;	DB 4;	Length 411;
Best Local Similarity	31.0%;	Pred. No. 7.4e-32;		
Matches 91;	Conservative 59;	Mismatches 102;	Indels 42;	Gaps 9

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QY      1 MKRNRVLAIVCTFTFYVLVGAAGFALAESEPELIRORLEIQQQLRARVNSOGYE 60
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      42 MKMKVSYIPLV--VLYLIIGATFVKALBEPHISQRTIIVIQKQFIISGHSVNS--T  97
QY      61 ELERVVLR-KPHKGV-----QWRPAGESYFALTITTTIGYGAABSDGKV 108
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      98 ELDELIDQIVAINAGIIGIPIGNTSNOQISHMDIGSSFPAGVITITTFGNGISPRTEGKI 157
QY     109 FCMFALIGPLPLVMPQSGEIRINTIVRYLLHRAKKGGLGRND-----VSM 166
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db     158 FCIYALIGLPEGFLAGVSDQGLTF-----GKGIAKEDYTFIKMNSQTKIRI 208
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY     157 ANMVLIGFSCISTLCIGAAAFSHYEHWTFEQAYYCYFTLTITTFGSDVYALQDAQLQT 216
      :::::|||||:::|||||:::|||||:::|||||:::|||||:::
Db     209 ISTIFILFEGCVLFAVLPALIFKHIEGMSALDAILYFVLTITTFGFDYVAGSD--IEY 266
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY     217 QPYAFSEFVYIILGTYIGAFMLV--VLRPMNMNDEKRD-AEHRALLTRN 267
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db     267 LDFKPVVMEIILVGLAFVAVLNSIGDWLVISKTKTEEGEERRAADEMTAN 320

```

```

: RESULT 3
: US-08-749-816-2
: Sequence 2, Application US/08749816
: Patent No. 6013470
: GENERAL INFORMATION:
: APPLICANT: Lesage, Florian
: APPLICANT: Guillemaire, Eric
: APPLICANT: Fink, Michel
: APPLICANT: Duprat, Fabrice
: APPLICANT: Lazdunski, Michel
: APPLICANT: Romey, Georges
: APPLICANT: Barnahin, Jacques
: TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS.
: TITLE OF INVENTION: THEIR CLONING AND THEIR USE ESPECIALLY FOR THE SCREENING
: OF DRUGS
: NUMBER OF SEQUENCES: 19
: CORRESPONDENCE ADDRESSES:
:

```

STREET : 230 South Fifteenth Street, Suite 500  
CITY : Philadelphia  
STATE : PA  
COUNTRY : USA  
ZIP : 19102  
COMPUTER READABLE FORM :  
MEDIUM TYPE : Floppy disk  
COMPUTER : IBM PC compatible  
OPERATING SYSTEM : PC-DOS/MS-DOS  
SOFTWARE : PatentIn Release #1.0, Version #1.3  
CURRENT APPLICATION DATA :  
APPLICATION NUMBER : US/08/749,816  
FILING DATE : 15-NOV-1996  
CLASSIFICATION : 536  
ATTORNEY/AGENT INFORMATION :

```

? NAME: Weiser, Gerard J.
? REGISTRATION NUMBER: 19,763
? REFERENCE/DOCKET NUMBER: 999.6351P
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 215-875-8383
? TELEFAX: 215-875-8394
? INFORMATION FOR SEQ ID NO: 2:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 336 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-08-749-816-2

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Query Match	15.7%	Score	320.5;	Length	336;
Best Local Similarity	32.4%;	Pred. No.	2.9;	Models	1;
Matches	90;	Conservative	47;	Mismatches	39;
				Gaps	9;

[illegible]

RESULT 4  
 : US-08-332-312-4  
 : Sequence 4, Application US/08332312  
 : Patent No. 5559026  
 : GENERAL INFORMATION:  
 : APPLICANT: Price, Laura A.  
 : APPLICANT: Pausch, Mark H.  
 : TITLE OF INVENTION: Functional Expression  
 : TITLE OF INVENTION: Melanagaster Putative  
 : NUMBER OF SEQUENCES: 4  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: American Cyanamid Company  
 : STREET: One Cyanamid Plaza  
 : CITY: Wayne  
 : STATE: New Jersey  
 : COUNTRY: US  
 : ZIP: 07470-8426  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: PatentIn Release #1.0, Versior  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/332,312  
 : FILING DATE:  
 : CLASSIFICATION: 435  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Harrington, James J.  
 : REGISTRATION NUMBER: P-38,711  
 : REFERENCE/DOCKET NUMBER: 37,421  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: 201-831-3246  
 : TELEFAX: 201-831-3305

Query match	11.38;	Score 231.5;	DB 1;	Length 618;
-------------	--------	--------------	-------	-------------

REGISTRATION NUMBER: 19,763  
REFERENCE/DOCKET NUMBER: 999.6351H  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-875-8383  
TELEFAX: 215-875-8394  
INFORMATION FOR SRD ID NO: 4:  
SEQUENCE CHARACTERISTICS:

LENGTH: 383 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-749-816-4

Query Match 9.3%; Score 190.5; DB 3; Length 383;  
 Best Local Similarity 24.0%; Pred. No. 9.8e-13;  
 Matches 62; Conservative 48; Mismatches 95; Indels 53; Gaps 9;

QY 11 LIVCTFYLLVGAVALDESEPELIERORLEKQOELRARY--NLSQG--GYEELE-- 63  
 DB 44 LVLSCTVYALGAYLFLSIHPELKRERKAREFDLKOQFMGNITSGIENSQSIET 103  
 QY 64 --RVVLRK-PHAGV-----QWRAGSFYFAITVITTTGCHAPSTDGK 107  
 DB 104 TKKLILMLEDAHNAHEEYFELNHEIIPKDMWTFSSALVFTTTVIPVGYIFPVSAVGR 163  
 QY 108 VFCMEYALGIPPLVWFQSLGERINTLVRYLLHRAKKGIGMRADVSMMNV----- 160  
 DB 164 MCLIALALLIPLVLTVMADTGKFAOLV-----TRWFGDNNMALPAAIFVCLLPAYP 216  
 QY 161 -LIGFSCISTLCIGAAAFSHYEHMTFFQAYYCYFTLTITIGFDYVALQDQALQTOPQ 219  
 DB 217 LVVGFILCSTS-----NITFLDSVYFSLISITIGFD--LPPDMNVHIMVL 261  
 QY 220 YVAFSPYIITGTVIGA 237  
 DB 262 FLAVGVLTITLDIVAA 279

RESULT 7  
 US-09-236-080-4  
 ; Sequence 4, Application US/09236080  
 ; Patent No. 6242217  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Helen Meadows  
 ; APPLICANT: Conrad Chapman  
 ; TITLE OF INVENTION: No. 6242217el Compounds  
 ; FILE REFERENCE: GP30031  
 ; CURRENT APPLICATION NUMBER: US/09/236,080  
 ; CURRENT FILING DATE: 1999-01-25  
 ; NUMBER OF SEQ ID NOS: 6  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 4  
 ; LENGTH: 107  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-236-080-4

Query Match 8.6%; Score 176.5; DB 4; Length 107;  
 Best Local Similarity 33.0%; Pred. No. 5e-12;  
 Matches 34; Conservative 22; Mismatches 26; Indels 21; Gaps 2;  
 QY 78 WRAGSFYFAITVITTTGCHAPSTDGKVFQMFVALLGIPPLVWFQSLGERINTLV 137  
 DB 9 WDLGSSFFAGYITTTGFGNISPRTEGKIFCIYALLIPLFGFLAGVGDQLGITF- 67  
 QY 138 YLLHRAKKGIGMRAD-----VSMANVILGFSFI 168  
 DB 68 -----GKGIKVEDTFIKMNVSQTKIRIISITIFILGCV 102

RESULT 8  
 US-08-749-816-3  
 ; Sequence 3, Application US/08749816  
 ; Patent No. 6013470  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lesage, Florian  
 ; APPLICANT: Guillemare, Eric

APPLICANT: Fluk, Michel  
 APPLICANT: Duprat, Fabrice  
 APPLICANT: Lazdunki, Michel  
 APPLICANT: Romey, Georges  
 APPLICANT: Barnhin, Jacques  
 TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS,  
 TITLE OF INVENTION: THEIR CLONING AND THEIR USE ESPECIALLY FOR THE SCREENING  
 NUMBER OF SEQUENCES: 19  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: WEISER & ASSOCIATES  
 STREET: 230 South Fifteenth Street, Suite 500  
 CITY: Philadelphia  
 STATE: PA  
 COUNTRY: USA  
 ZIP: 19102  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk.  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: patentin Release #1.0, Version 1.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/749,816  
 FILING DATE: 15-NOV-1996  
 CLASSIFICATION: 536  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Weiser, Gerard J.  
 REGISTRATION NUMBER: 19,763  
 REFERENCE/DOCKET NUMBER: 989.6351P  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 215-875-8383  
 TELEFAX: 215-875-8394  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 347 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-749-816-3

Query Match 7.6%; Score 156; DB 3; Length 347;  
 Best Local Similarity 22.6%; Pred. No. 5.7e-05;  
 Matches 52; Conservative 45; Mismatches 10; Indels 36; Gaps 6;

QY 3 RQVRLALIVCTFYLL--LVGAVALDESEPELIERQ ELRQOELRARNLSOGY 59  
 DB 31 RQVNVVVCISAATILVFNLIAGIFLYAETQ--SSSE; NENSEVSKLHNPIG- 86  
 QY 60 EELERVVLRKPH-----KAGVQWPFAGSFYFAITVITTTI VGHAPSTDGKVCMPY 113  
 DB 87 -----KITAEKSKLKGCLKRSRIDGFKAIFFSWLYSVYGLSPHSTLGRYITTY 142  
 QY 114 ALLGIPPLVWFQSLGERINTLVRYLLHRAKKGIGMRADVSMMAN----- 158  
 DB 143 SLIMIPVFIAKFEFGTFLAHFLVAVSNRTR--LAVKAVYKLSQBPENAEPPSNLSQHD 200  
 QY 159 --RVVLFSCISTLCIGAAAFSHYEHMTFFQAYYCYFTLTITIGFDY 206  
 DB 201 YLIFSSLLCISLSSSALFSSISNISVSVYGIITMFLIGDVI 250

RESULT 9  
 US-08-288-405A-10  
 ; Sequence 10, Application US/08288405A  
 ; Patent No. 5559009  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Chandu, Kaulanthara G.  
 ; APPLICANT: Kaiman, Katalin  
 ; APPLICANT: Chandu, Grischu  
 ; APPLICANT: Gutman, George A.  
 ; TITLE OF INVENTION: A NO. 5559009el Voltage-gated Potassium Channel



TITLE OF INVENTION: Gene  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESS: Flehr, Hohbach, Test, Albritton & Herbert,  
ATTORNEYS: Altn: Walter H. Dreger  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: United States  
ZIP: 94111-4187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/288,405A  
FILING DATE: 10-AUG-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/207,431  
FILING DATE: 04-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Dreger, Walter H.  
REGISTRATION NUMBER: 24,190  
REFERENCE/DOCKET NUMBER: A-59844-1/WHD  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 781-1989  
TELEFAX: (415) 398-3249  
TELEX: 910 277299  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 532 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-288-405A-10

Query Match 5.0%; Score 103; DB 1; Length 532;  
Best Local Similarity 22.8%; Pred. NO. 0.0085;  
Matches 34; Conservative 27; Mismatches 36; Indels 52; Gaps 7;

QY 3 RQNVETLALIVCTFTYLLVGAAPDALESEPELLERORLELROELRARNYLSOGGYEEL 62  
DB 382 RASMELEGLIT---SELPITGVLFSS-----AVY-----FAEV 411  
QY 63 EERVLRKPKHAGVQWRPAGSFYFAITVITTTIGYGHAA PSTDGGKVFCEMFAALLGI 118  
DB 412 DRV---DTHEFSI---PESEFMVAIVMTTIVGYGDMA PVTVGKIVGSLAIAVLFTIS 463  
QY 119 -PLTIVMFSQISGERINTLVRYLLHRAKKG 146  
DB 464 LPPVPIV-----SNFSYFYHRETEG 483

RESULT 10  
Sequence 2, Application US/08956242C  
Patent No. 5986081  
GENERAL INFORMATION:  
APPLICANT: Ganetzky, Barry S.  
TITLE OF INVENTION: Polynucleotides Encoding Herg-3  
FILE REFERENCE: 960296.94550  
CURRENT APPLICATION NUMBER: US/08/956,242C  
CURRENT FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 2  
LENGTH: 626  
TYPE: PRT  
ORGANISM: Homo sapien

FEATURE:  
NAME/KEY: unsure  
LOCATION: (441)..(542)  
OTHER INFORMATION: unidentified at time of filing  
US-08-956-242-2

Query Match 5.0%; Score 102.5; DB 2; Length 626;  
Best Local Similarity 23.7%; Pred. NO. 0.012;  
Matches 33; Conservative 32; Mismatches 4; Indels 29; Gaps 5;

QY 9 LALIVCTFTYLLVGAAPDALESEPELLERORLEL---OOELRARNYLSOGGYE 60  
DB 274 LFLMCTFALLAHMLACIMYAIQN---VERPYLEHKIGM SLAVOLGKRYNGSD---- 325  
QY 61 EERVLRKPKHAGVQWRPAGSFYFAITVITTTIGYGHAA PSTDGGKVFCEMFAALLGIPL 120  
DB 326 -----PASGPSVQOKYVYALYFTFSSILTSVGFQNV---NFTNSEKVFSLICVMLIG--- 373  
QY 121 TLVMPFSQISGERINTLVRYL 139  
DB 374 -SLMVASIFGNVSAIIORL 391

RESULT 11  
Sequence 2, Application US/09351215  
Patent No. 6087468  
GENERAL INFORMATION:  
APPLICANT: Ganetzky, Barry S.  
TITLE OF INVENTION: Polynucleotides Encoding Herg 3  
FILE REFERENCE: 960296.94550  
CURRENT APPLICATION NUMBER: US/09/351,215  
CURRENT FILING DATE: 1999-07-12  
EARLIER APPLICATION NUMBER: 08/956,242  
EARLIER FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 2  
LENGTH: 626  
TYPE: PRT  
ORGANISM: Homo sapien  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (441)..(542)  
OTHER INFORMATION: unidentified at time of filing  
US-09-351-215-2

Query Match 5.0%; Score 102.5; DB 4; Length 626;  
Best Local Similarity 23.7%; Pred. NO. 0.012;  
Matches 33; Conservative 32; Mismatches 4; Indels 29; Gaps 5;

QY 9 LALIVCTFTYLLVGAAPDALESEPELLERORLEL---OOELRARNYLSOGGYE 60  
DB 274 LFLMCTFALLAHMLACIMYAIQN---VERPYLEHKIGM SLAVOLGKRYNGSD---- 325  
QY 61 EERVLRKPKHAGVQWRPAGSFYFAITVITTTIGYGHAA PSTDGGKVFCEMFAALLGIPL 120  
DB 326 -----PASGPSVQOKYVYALYFTFSSILTSVGFQNV---NFTNSEKVFSLICVMLIG--- 373  
QY 121 TLVMPFSQISGERINTLVRYL 139  
DB 374 -SLMVASIFGNVSAIIORL 391

RESULT 12  
Sequence 4, Application US/08464340A  
Patent No. 5710019  
GENERAL INFORMATION:  
APPLICANT: LI, ET AL.

```

1 TITLE OF INVENTION: Human Potasslum Channel 1 and 2 Proteins
2 NUMBER OF SEQUENCES: 13
3 CORRESPONDENCE ADDRESS:
4 ADDRESSEE: CARELLA, BYRNE, BAIN, GIEFFLAN,
5 ADDRESSEE: CECCHI, STEWART & OLSTEIN
6 STREET: 6 BECKER FARM ROAD
7 CITY: ROSELAND
8 STATE: NEW JERSEY
9 COUNTRY: USA
10 ZIP: 07068
11 COMPUTER READABLE FORM:
12 MEDIUM TYPE: 3.5 INCH DISKETTE
13 COMPUTER: IBM PS/2
14 OPERATING SYSTEM: MS-DOS
15 SOFTWARE: WORD PERFECT 5.1
16 CURRENT APPLICATION DATA:
17 APPLICATION NUMBER: US/08/464,340A
18 FILING DATE: June 5, 1995
19 CLASSIFICATION: 435
20 PRIOR APPLICATION DATA:
21 APPLICATION NUMBER: PCT/US94/08449
22 FILING DATE: 28 JUL 1994
23 ATTORNEY/AGENT INFORMATION:
24 NAME: FERRARO, GREGORY D.
25 REGISTRATION NUMBER: 36,134
26 REFERENCE/DOCKET NUMBER: 325800-415
27 TELECOMMUNICATION INFORMATION:
28 TELEPHONE: 201-994-1700
29 TELEFAX: 201-994-1744
30 INFORMATION FOR SEQ ID NO: 4:
31 SEQUENCE CHARACTERISTICS:
32 LENGTH: 494 AMINO ACIDS
33 TYPE: AMINO ACID
34 STRANDEDNESS:
35 TOPOLOGY: LINEAR
36 MOLECULE TYPE: PROTEIN
37 US-08-464-340A-4

```

1 TITLE OF INVENTION: Potassium Channel Protein I and 2  
2  
3 NUMBER OF SEQUENCES: 4  
4 CORRESPONDENCE ADDRESS:  
5  
6 ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
7  
8 ADDRESSEE: CECCHI, STEWART & OLSTEIN  
9  
10 STREET: 6 BECKER FARM ROAD  
11  
12 CITY: ROSELAND  
13  
14 STATE: NEW JERSEY  
15  
16 COUNTRY: USA  
17  
18 ZIP: 07068  
19  
20 COMPUTER READABLE FORM:  
21  
22 MEDIUM TYPE: 3.5 INCH DISKETTE  
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24 COMPUTER: IBM PS/2  
25  
26 OPERATING SYSTEM: MS-DOS  
27  
28 SOFTWARE: WORD PERFECT 5.1  
29  
30 CURRENT APPLICATION DATA:  
31  
32 APPLICATION NUMBER: PCT/US94/08449A  
33  
34 FILING DATE: SUBMITTED HEREWITH  
35  
36 CLASSIFICATION:  
37  
38 PRIOR APPLICATION DATA:  
39  
40 APPLICATION NUMBER:  
41  
42 FILING DATE:  
43  
44 ATTORNEY/AGENT INFORMATION:  
45  
46 NAME: FERRARO, GREGORY D.  
47  
48 REGISTRATION NUMBER: 36,134  
49  
50 REFERENCE/DOCKET NUMBER: 325800-105  
51  
52 TELECOMMUNICATION INFORMATION:  
53  
54 TELEPHONE: 201-994-1700  
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56 TELEFAX: 201-994-1744  
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60 SEQUENCE CHARACTERISTICS:  
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62 LENGTH: 494 AMINO ACIDS  
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64 TYPE: AMINO ACID  
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66 STRANDEDNESS:  
67  
68 TOPOLOGY: LINEAR  
69  
70 MOLECULE TYPE: PROTEIN  
71  
72 PCT-US94-08449A-4

1	APPLICANT: Ganetzky, Barry S.	
2	APPLICANT: Titus, Steven A.	
3	TITLE OF INVENTION: Polynucleotides Encoding Herg-3	
4	FILE REFERENCE: 960296, 94550	
5	CURRENT APPLICATION NUMBER: US/08/956, 242C	
6	CURRENT FILING DATE: 1997-10-22	
7	NUMBER OF SEQ ID NOS: 13	
8	SOFTWARE: PatentIn Ver. 2.0	
9	SEQ ID NO 4	
10	LENGTH: 868	
11	TYPE: PRT	
12	ORGANISM: Homo sapien	
13	FEATURE:	
14	NAME/KEY: unsure	
15	LOCATION: (133)	
16	OTHER INFORMATION: Unidentified at time of filing	
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66	NAME/KEY: unsure	
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1 NAME/KEY: unsure
2 LOCATION: (611)
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5 NAME/KEY: unsure
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46 LOCATION: (661)
47 OTHER INFORMATION: Unidentified at time of filling
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49 NAME/KEY: unsure
50 LOCATION: (662)
51 OTHER INFORMATION: Unidentified at time of filling
52 US-08-956-242-4
53
54 Query Match 4.9% Score 99.5; DE:2 Length 888;
55 Best Local Similarity 19.5% Pred. NO. 0.045
56 Matches 31; Conservative 34; Mismatches 15; Indels 49; Gaps 6
57
58 QY 46 QELRAYNLSSGGVEELERVVLRKPKHAGVOMRFGSPHYAIVITITGVGHAPSPDG 105
59 DB 236 QOIGRRINDSSSS-----SGPSTKDKVTAL\ITFSSLTSGFGVNSPNTNS 282
60 QY 106 GKVECFMAYLGIPLTVMFQSLGERINTLVRYL-----LHRAKKG 146
61 DB 283 EKISICMVLG---SLMTVASIFGVNSAIIORLKSQTA\AKOMLRVKEFIRFQIPNP 338
62 QY 147 LGMRRAD-----VSMANMYLIGFFSCI-STLCI 173
63 DB 339 LRRRLLEEFQHAMVTYNGIDM-NMYLKGFPECLQADIC\ 35

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RESULT 15  
US-09-351-215-4  
Sequence 4, Application US/09351215  
Patent No. 6087488  
GENERAL INFORMATION:  
APPLICANT: Ganetzky, Barry S.  
APPLICANT: Titus, Steven A.  
TITLE OF INVENTION: Polynucleotides Encoding Herg-3  
FILE REFERENCE: 960296 94550  
CURRENT APPLICATION NUMBER: US/09/351,215  
CURRENT FILING DATE: 1999-07-12  
EARLIER APPLICATION NUMBER: 08/956,242  
EARLIER FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: Patentln Ver. 2.0  
SEQ ID NO 4  
LENGTH: 888  
TYPE: PRT  
ORGANISM: Homo sapien  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (133)  
OTHER INFORMATION: Unidentified at time of filing  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (181)  
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NAME/KEY: unsure  
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OTHER INFORMATION: Unidentified at time of filing  
US-09-351-215-4

Query Match 4.9%; Score 99.5; D: 3; Length 888;  
Best Local Similarity 19.5%; Pred No 0.045;  
Matches 31; Conservative 34; Mismatches 45; Indels 49; Gaps 6;  
OY 46 QELRARNLSGGYELRLRVLRKPKAGVOWRFGSI-A-VITIGYGHAPSTDG 105  
::: ||| |  
::: |  
::: |



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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd

OM protein - protein search, using sw model

Run on: August 28, 2001, 17:07:05 ; Search time 36.66 Seconds  
(Without alignments)  
818.679 Million cell updates/sec

Title: US-09-503-089A-5  
Perfect score: 2042

Sequence: 1 MKRQNVRLALIVCTFTYLL.....STGLHSLSTFRGLMKRRSSV 394

Scoring table:	BLOSUM62	Canoe	0.5
	Canoe	10	0

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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**Pred. No.** is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	820	40.2	339	2	T43509	probable potassium outward rectifier
2	806.5	39.5	2	T32347	hypothetical prote	
3	599	29.3	334	2	T19860	probable potassium inward rectifier p
4	599	29.3	364	2	T43361	hypothetical prote
5	320.5	15.7	336	2	S65566	hypothetical prote
6	307.5	15.1	513	3	T28933	hypothetical prote
7	293	14.3	393	2	T25392	hypothetical prote
8	275	13.5	524	2	T23907	hypothetical prote
9	268	13.1	1539	2	T30037	hypothetical prote
10	262	12.8	443	2	T21598	potassium channel
11	261.5	12.8	1001	2	T13807	f22b7.7 protein -
12	259.5	12.7	335	2	S44535	hypothetical prote
13	258.5	12.7	427	2	T27681	hypothetical prote
14	258	12.6	383	2	T23182	hypothetical prote
15	256.5	12.6	452	2	T21118	potassium channel
16	251	12.3	544	2	T43364	potassium channel
17	251	12.3	576	2	T43363	probable potassium
18	250	12.2	569	2	T43531	hypothetical prote
19	248	12.1	444	2	T26229	hypothetical prote
20	247.5	12.0	392	2	T45032	hypothetical prote
21	245	12.0	769	2	T27550	hypothetical prote
22	244	11.9	381	2	T43393	potassium channel
23	243	11.9	528	2	T21834	hypothetical prote
24	239.5	11.7	522	2	T24265	hypothetical prote
25	235.5	11.5	475	2	T27725	hypothetical prote
26	234.5	11.5	485	2	T24301	hypothetical prote
27	231.5	11.3	484	2	T43529	probable potassium
28	231.5	11.3	519	2	T16529	hypothetical prote
29	229	11.2	325	2	T15584	hypothetical prote

30	229	11.2	461	2	T43394	potassium channel
31	222.5	10.9	600	2	T24626	hypothetical prote
32	216	10.6	350	2	T15178	hypothetical prote
33	215.5	10.6	643	2	T26616	hypothetical prote
34	211	10.3	539	2	T23700	hypothetical prote
35	210.5	10.3	504	2	T23269	hypothetical prote
36	210	10.3	1136	2	T26953	hypothetical prote
37	205.5	10.1	586	2	T21683	hypothetical prote
38	201.5	9.9	551	2	T16426	hypothetical prote
39	201.5	9.9	555	2	T43357	potassium channel
40	199.5	9.8	700	2	T27364	hypothetical prote
41	199.5	9.8	660	2	T21551	hypothetical prote
42	193.5	9.5	523	2	T23373	hypothetical prote
43	190.5	9.3	383	2	T23746	hypothetical prote
44	189.5	9.3	631	2	T26232	hypothetical prote
45	185	9.1	681	2	T19429	hypothetical prote

## ALIGNMENTS

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RESULT      1
T43509
probable potassium channel chain n2P38 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000
C:Accession: T43509
R:Mang, Z.W.; Salcoff, L.
submitted to the EMBL Data Library, August 1998
A:Description: Potassium channels in C. elegans.
A:Reference number: Z22450
A:Accession: T43509
A>Status: preliminary; translated from GB/EMBL/DDP
A:Molecule type: mRNA
A:Residues: 1-329 <MAN>
A:Cross-references: EMBL:AF083652; PIDN:AAC32863.4

Query Match          40.2%   Score 820; DDP Length 329;
Best local similarity 48.3%; Pred. No. 3.1e
Matches 172; Conservative 54; Mismatches 14; Indels 46; Gaps

OY      1 MKROVPTLATLVCFPTLLVGAAPFDALSEPELEK...HROELRLARYNLQSGYE 60
Db       1 MKRKIRLSLVCLVTLLVLGAAFPDALETNELORF...RVREKLTKTNMSNADE 60
        | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY      61 ELERVLYLRKPRAQVQRPAQSFFYAIVTTITIGYH...ETDGGKYFCMFYALLGIPL 120
Db       61 ILEATIVKSPVRKAGYQMKFGCAFYFAATVITTYIGH...IDAGKVCMLYALAGIPL 120
        | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY     121 TLVMQSLGERINTLVRLILRAKKGLGRADVSMAN...TFPSICSTLCI--GAAAF 178
Db     121 GLIMQSLGERINNTFAAKLRFRIIRAAG-KOPIVASSD...FCTGMGGLIFGGAFAF 177
        | | | | | | | | | | | | : | : | : | : | : | : | : | : |
OY     179 SHYHEPFEOAYVCEIFLTITGFDDVALOKDALOT...YVARSPYILGLNVIGAF 238
Db     178 SYEHWITFDVAIVYCFVTLITTGFDVIYALKRGSLQT...VFPSLVPIFLGLVVISNA 237
        | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY     239 LNLVYLRTPMNAEDKEKDARHAL----LTRNGOAGG...GSAAHTDTFASSTAAGG 294
Db     238 MNLLVLRRLTMNTEBERRDGEAILLAAGLVAVGPNTL DGRILPLDSNVSLAS----- 292
        | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY     295 GFRNVAYEVLFQSKSCCIWYSRKREKLOYSTIPMIIPRI...MHNPCVEOSHSSPGGG 350
Db     293 -----CSC-YQLPDPEKLRHR-----HHKHTEPHHG 316
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RESULT      2
T43247
outward rectifier potassium channel homolog twk-2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999
C:Accession: T43247

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R:Muray, J.; Wohldmann, P.; O'Neal, D.  
Submitted to the EMBL Data Library, September 1997  
A:Description: The sequence of C. elegans cosmid F34D6.  
A:Reference number: Z21153

A:Accession: T32347  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-336 <MUR>  
A:Cross-references: EMBL:AF025454; PIDN:AC71151.1; GSPDB:GN00020; CESP:F34D6.3  
A:Experimental source: strain Bristol N2; clone F34D6  
A:Gene: twk-23; CESP:F34D6.3  
A:Map position: 2  
A:Introns: 44/3; 102/1; 136/1; 180/1; 207/1; 265/2; 296/3

Query Match 39.5%; Score 806.5; DB 2; Length 336;  
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QY 54 LSQGYEELERVVLRKPKRAGVQMRPAGSEFYFAITVITIGYGAAPSTDCGKPCMFY 113  
DB 61 MSNADYILERTIVKSVPHKAGYQMKFSGAFYFATVITIGYHSTPMIDAGVFCMLY 120  
QY 114 ALGIPPLTVFOSLGRINTLVRYLLHRKKGIGMRADVSMANVLLGFSCISTLCT 173  
DB 121 ALADIPGLIMFOSIGGRMTFAKLLRFRRAAG-KQPIVTSDDLII--FCTGMCGLLI 177  
QY 174 --GAAASHEHMTFFQAYYCFITLTIGFDVVALOKOALOTOPQYAFSVYLLTG 231  
DB 178 FCGAFMSSSTENTYTFAYVYCFITLTIGFDVVALOKGSLTOPEYVFFSLVFLFG 237  
QY 232 LTVIGAFNLVLRKMTMAEDEKRAEHRAL----LTRNGOAGGGGSAHTTDTASS 287  
DB 238 LTVISAMNLLVLRFLMTNTERDEQEAIIAAGLVRVGDPTADDFGLPLSDNVSL 297  
QY 288 TAAAGGGGFRRNVAEVLFHOSMGCLMYKSRKLOYSIPMIIPDLSTSDTCVQSHSSP 347  
DB 298 AS-----CSC-YQLPDEKLRH-----HRKHTEP 320  
QY 348 GGG 350  
DB 321 HGG 323

RESULT 3  
T19860  
hypothetical protein C40C9.1 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000  
C:Accession: T19860  
R:Hemby, C.  
Submitted to the EMBL Data Library, March 1996  
A:Reference number: Z19188  
A:Accession: T19860  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-334 <WIL>  
A:Cross-references: EMBL:Z70266; PIDN:CAA94204.1; GSPDB:GN00028; CESP:C40C9.1  
A:Experimental source: clone C40C9  
A:Gene: CESP:C40C9.1  
A:Map position: X  
A:Introns: 34/1; 60/2; 98/1; 145/3; 160/3; 181/1; 204/1; 252/2; 279/2; 306/3

Query Match 29.3%; Score 599; DB 2; Length 334;  
Best Local Similarity 46.1%; Pred. No. 5.1e-47;  
Matches 119; Conservative 46; Mismatches 81; Indels 12; Gaps 3;

QY 4 ONVRTALIVCTFTYLLVGAAVFDALSEPELLRORLEI--KOLRARNVLSQGYEEL 63  
DB 7 KSARALLILSTFTYLLFGAMVFDKLESEKDTWRDEIEFI--DLRKHYKVFSEDLHFE 66  
QY 64 RYVLRKPKRAGVQMRPAGSEFYFAITVITIGYGAAPSTDCGKPCMFY 123  
DB 67 AIAIKSIPQOAGYQWQAGAFYFATVITIGYGHSP--INACKLFCMIFALGVPMLI 126  
QY 124 MFSLSGRINTLVRYLLHRKKGIGMR----RADVSMANVLL--IGFSCISTLCTGA 175  
DB 127 MFSLSGRINTLVRYLLHRKKGIGMR----RADVSMANVLL--IGFSCISTLCTGA 182  
QY 176 AARSHEHMTFFQAYYCFITLTIGFDVVALOKOAL--TOQYAFSVYLLTGTVI 235  
DB 183 YMFHTIEKMSIFDYYFCMTFTSTIGFGDLVPLQVNVN--LYVFATIMFLIGLAVF 242  
QY 236 GAFNLVLRKMTMAED 253  
DB 243 SACCNVLLVLFMSNAD 260

RESULT 4  
T43361  
probable potassium channel chain n2p20 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 11-Jan-2000  
C:Accession: T43361  
R:Wang, Z.W.; Salkoff, L.  
Submitted to the EMBL Data Library, August 1998  
A:Description: Potassium channels in C. elegans.  
A:Reference number: Z22450  
A:Accession: T43361  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-364 <MAN>  
A:Cross-references: EMBL:AF083646; PIDN:AC32857.1

Query Match 29.3%; Score 599; DB 2; Length 364;  
Best Local Similarity 46.1%; Pred. No. 5.7e-48;  
Matches 119; Conservative 46; Mismatches 81; Indels 12; Gaps 3;

QY 4 ONVRTALIVCTFTYLLVGAAVFDALSEPELLRORLEI--KOLRARNVLSQGYEEL 63  
DB 7 KSARALLILSTFTYLLFGAMVFDKLESEKDTWRDEIEFI--DLRKHYKVFSEDLHFE 66  
QY 64 RYVLRKPKRAGVQMRPAGSEFYFAITVITIGYGAAPSTDCGKPCMFY 123  
DB 67 AIAIKSIPQOAGYQWQAGAFYFATVITIGYGHSP--INACKLFCMIFALGVPMLI 126  
QY 124 MFSLSGRINTLVRYLLHRKKGIGMR----RADVSMANVLL--IGFSCISTLCTGA 175  
DB 127 MFSLSGRINTLVRYLLHRKKGIGMR----RADVSMANVLL--IGFSCISTLCTGA 182  
QY 176 AARSHEHMTFFQAYYCFITLTIGFDVVALOKOAL--TOQYAFSVYLLTGTVI 235  
DB 183 YMFHTIEKMSIFDYYFCMTFTSTIGFGDLVPLQVNVN--LYVFATIMFLIGLAVF 242  
QY 236 GAFNLVLRKMTMAED 253  
DB 243 SACCNVLLVLFMSNAD 260

RESULT 5  
S65566  
inward rectifier potassium channel TWIK-1 - human  
C:Species: Homo sapiens (man)  
C>Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 05-Nov-1999  
C:Accession: S65566  
R:Lesage, F.; Guillemare, E.; Fink, M.; Duprat, C.; Lazdunski, M.; Romey, G.; Barhan  
EMBL J. 15, 1004-1011, 1996  
A:title: TWIK-1, a ubiquitous human weakly inward rectifying K(+) channel with a nove





A:Reference number: 219816  
 A:Accession: T23907  
 A>Status: preliminary; translated from GB/EMBL/DBD  
 A:Molecule type: DNA  
 A:Residues: 1-524 <MIL>  
 A:Cross-references: EMBL:Z74475; PIDN:CAA98957.1; GSPDB:GN00023; CESP:F04F11.4  
 A:Experimental source: clone R04F11  
 C:Genetics:  
 A:Gene: CESP:R04F11.4  
 A:Map position: 5  
 A:Introns: 35/3; 83/2; 131/1; 170/1; 261/1; 306/1; 338/1; 369/1; 489/2

Query Match 13.5%; Score 275; DB 2: Length 524;  
 Best Local Similarity 23.9%; Pred. No. 3.8e-17;  
 Matches 88; Conservative 38; Mismatches 92; Indels 150; Gaps 9;

QY 11 LIVCTFTYLLVGAADFALDESEPELIERORLEKQOELRARY-----52  
 DB 18 LVLLISYVTLIGALCFHNEYEQQLNETSRIGELKRNVDQLWRMSNGTASTWR 77  
 QY 53 NLGGGEELERVY-----RLKPH-----KAGVORFAGSFPAITVITIGYGAAP 101  
 DB 78 QTADGMDDELROVEMDYTRNMPDDVIYGDGPIKMSFMSISFMTATITIGYGHIVP 137  
 QY 102 STDGKVFCEFYALLGIPILVFMFOSLGERINTLV-----136  
 DB 138 RTDGRVAIIFFYALGIPILVITADIGRFLATYIIKLHGMAVMSFVNSCLKCIKMA 197  
 QY 137 -----RY-----LLHRAKK-----GLGMR-----150  
 DB 198 CCMVRLPRRHIPMTLELLQRTOKLYPNNNPVAATAASGGGTGRKKQQRDNVSDAG 257  
 QY 151 -----RADYSMANMVLIGFSCSTICIG 174  
 DB 258 TFDNISINDSGEGENEGEEEOIQDPPSNEKRVSVLEFILLMLGY-----VAGG 311  
 QY 175 AAASFHEHTFEOAYYCFITLTITGFGYVALQKDAOTOPQYVAFSFTVLTGLTV 234  
 DB 312 AYIYRMWEMTFEAFYFCFVTVTITIGFDIVPANVD-----WLPATLAIYVFLII 363  
 QY 235 IGAFLNLY 242  
 DB 364 TTMCIDLV 371

RESULT 9

T30037  
 hypothetical protein F20A1.7 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C:Accession: T30037  
 R:Gating: S; Wu, X.  
 submitted to the EMBL Data Library, March 1996  
 A:Description: The sequence of C. elegans cosmid F20A1.  
 A:Reference number: Z20726  
 A:Accession: T30037  
 A>Status: preliminary; translated from GB/EMBL/DBD  
 A:Molecule type: DNA  
 A:Residues: 1-1539 <GAT>  
 A:Cross-references: EMBL:U053150; PIDN:AAA96127.1; GSPDB:GN00023; CESP:F20A1.7  
 A:Experimental source: strain Bristol N2; clone F20A1  
 C:Genetics:  
 A:Gene: CESP:F20A1.7  
 A:Map position: 5  
 A:Introns: 19/3; 41/2; 71/2; 110/3; 135/2; 190/1; 246/1; 287/3; 491/3; 598/2; 983/2; 110

Query Match 13.1%; Score 268; DB 2: Length 1539;  
 Best Local Similarity 24.6%; Pred. No. 6.2e-16;  
 Matches 96; Conservative 60; Mismatches 126; Indels 108; Gaps 13;

QY 8 TLALVCTFTYLLVGAADFALDESEPELIERO-----RLLEKQOELRA-RYNLSGGG 58

DB 88 TFKLLIIGLYSGIAHIFVLEVPDLEAREDFHQRIKLVYMLNLALFIYDNRNEDR 147  
 QY 59 YEELERVVLRKPKHAKGVQ-----WRFAGSFYFAITVITIGYGAAPSTDGKVFCEM 111  
 DB 148 EEMKRAHILKFE-EDIGLEBPVIEIETVTFMMSFLYAGTII-IGYGNACKTRAGOTATM 206  
 QY 112 FYALLGIPILVFMFOSL-----132  
 DB 207 VYAFVGIPILVMTLSINNFLAKMIKLITNGVSDMTLYTC-AGIYIRODEVOKRLRT 266  
 QY 133 ---NTLVRYLL--HRAKKGMRADYSMANM-----VLIGFSCISTL 171  
 DB 267 KLAKTMRKRLSKHGAAPSAISNSEENRLNSPDEDI-CHODPPVSLTIATYAWI 326  
 QY 172 CIGAAAFHEHTFEOAYYCFITLTITGFGYVALQ-MAOTOPQYVAFSFTVLTGLTV 231  
 DB 327 ILSAAVFCLEFEDWTFEFSFCEISLTITIGLD-----VTPANDEVMAIATFGVIYG 378  
 QY 232 LVYIYGAFLNLVLRPMTWNADEKRDRAHRALLTRNCG-AGGGGSAHTTDTASTAA 291  
 DB 379 LSMITVCIDVLOEKLAOMY-----ALLOKLITYM-----DPNAAASAMA 425  
 QY 292 GGGG-----FRNYAEVL-HFQSMCS 311  
 DB 426 GFGGRAKFLMPLLSKNEGAKVMDKFKODCS 455

RESULT 10

T21598  
 hypothetical protein F31D4.7 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-19  
 C:Accession: T21598  
 R:Kortliffe, B.  
 submitted to the EMBL Data Library, March 1997  
 A:Reference number: Z19447  
 A:Status: preliminary; translated from GB/EMBL/DBD  
 A:Molecule type: DNA  
 A:Residues: 1-443 <MIL>  
 A:Cross-references: EMBL:Z92832; PIDN:CAB07375.1; GSPDB:GN00023; CESP:F31D4.7  
 A:Experimental source: clone F31D4  
 C:Genetics:  
 A:Gene: CESP:F31D4.7  
 A:Map position: 5  
 A:Introns: 13/3; 90/2; 149/1; 222/3; 290/3

Query Match 12.8%; Score 262; DB 2: Length 443;  
 Best Local Similarity 25.0%; Pred. No. 4.7e-16;  
 Matches 78; Conservative 55; Mismatches 113; Indels 66; Gaps 9;

QY 11 LIVCTFTYLLVGAADFALDESEPELIERORLEKQOELRARNLSQ-----56  
 DB 17 LIVFLIYCISGGLVFWLIEPYOELRDAMQHKIENNRFARVDAMMKKIFNNSDYLIYI 76  
 QY 57 -----CGYELEERVVLRKPKHAGVORFAGSFYFAITVITIGYGAAP 100  
 DB 77 KGNTSORLTTFTFEEIGSYEN---QIGVAKWSQOKMDWVWNLVAGTCTTIGYGHY 132  
 QY 101 PSTDGKVFCEFYALLGIPILVFMFOSLGERINTLVYLLHFAKKGL-----147  
 DB 133 PMTDAGMLMTFALRCEIPLMLLVLDQFGLLITITMKFPWFOIKRLMRRIMRCTOPIE 192  
 QY 148 -----GMRADYSMANMVL-IGFSCISTPLCIGAAAFSNEYH-WTFEQAYYCFITLT 199  
 DB 193 EMKEIEROERHDDIDPLPVPVAGIALVTWIFICSFVLSVNDHNMWLTLESFYEFTSLST 252  
 QY 200 IGGGDYVALQKDAOLQOPQYVAFSFTVLTGLTVIGN-ANVLRPMT---ANADEKR 256  
 DB 253 VGLGDIV-----PSSPRLITMGEFILLVGLSVSN-INTLOAKKSTYEAGRNDEKT 304



A:Accession: T23182  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-383 <MIL>  
 A:Cross-references: EMBL:275543; PIDN:CAA99871.1; GSPDB:GN00023; CESP:K01D12.4  
 A:Experimental source: clone K01D12  
 C:Genetics:  
 A:Gene: CESP:K01D12.4  
 A:Map position: 5  
 A:Introns: 28/3; 76/3; 184/2; 217/2; 270/2; 295/2

Query Match 12.6%; Score 258; DB 2; Length 383;  
 Best local similarity 25.6%; Pred. No. 9.2e-16;  
 Matches 77; Conservative 57; Mismatches 113; Indels 54; Gaps 8;

QY 4 QNRTLALVCTFTYLLVGAADFALSEPELIERQRLERQDELRLARY----NLSGGY 59  
 DB 40 ENAREVLIICILIVLAFALFHLMEWENEVERIAIDRMADYQVCKHKLNECDF 99  
 QY 60 EELERVVLRLKPKAGV-----QMRPAGSFYFAIVYTTTGYGAAPSTDGKVFQCMFYA 114  
 DB 100 EEMVRFI--SDGATSGILNSRFRDHLGLFSATVISTIGFSTPRTHLGRFTIYVG 157  
 QY 115 LGLPIPLVNFQSLGERINTLVRYL-----HRAKK----- 145  
 DB 158 VVGCTCCVLFENFLERLVGMSYILSLRERKIRYRLKESGNKPVTLINNEDENESS 217  
 QY 146 --GLGMRADVSANVNLGFFSCISTICGAAPSHYEHMTFQAVYVCEITLTITGFG 203  
 DB 218 SCGGHMDNRPSPYKVFILFSMCLVLTASAGIYSVENMNYIDSLYFCFISFATIGFG 277  
 QY 204 DYVALQKDALQTOPQY-----VAESFYILTGLT--VIGAFNLVLRFMTMAE 252  
 DB 278 DYVSNQDDVTBMSPDLYRFNFCLLTLGACFFCLSNVSSIIVRQLNMIMKK-MDYKVE 336  
 QY 253 D 253  
 DB 337 D 337

RESULT 15  
 T23118  
 hypothetical protein F19D8.1 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000  
 C:Accession: T23118  
 R:Swindburne, J.; Almscough, R.  
 submitted to the EMBL Data Library, August 1996  
 A:Reference number: Z19377  
 A:Accession: T23118  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-452 <MIL>  
 A:Cross-references: EMBL:278541; PIDN:CAB01740.1; GSPDB:GN00028; CESP:F19D8.1  
 A:Experimental source: clone F19D8  
 C:Genetics:  
 A:Gene: CESP:F19D8.1  
 A:Map position: X  
 A:Introns: 31/1; 82/2; 101/3; 157/1; 197/1; 230/3; 267/2; 325/3; 356/1; 404/3

Query Match 12.6%; Score 256.5; DB 2; Length 452;  
 Best local similarity 28.6%; Pred. No. 1.5e-15;  
 Matches 82; Conservative 47; Mismatches 91; Indels 67; Gaps 12;

QY 1 MKRQNVRLAL-----IVCTFTYLLVGAADFAL--ESEPELIERQ--LELRQ-- 46  
 DB 36 MKFRNVRLALGHALYCFVVC--YVFAGAWFHQLEGENETELHDKQREYAMNLKKDY 92  
 QY 47 --ELRARIYLSGGYEELERVLR-----LKPDKAGVQMRFAGSF 84  
 DB 93 IAKLATTEENVAE--INEHLMFLRNISNLHISIDNYLIENEPQIVPKR---WTFPSSV 146

QY 85 YFAITVITTYGYGAAPSTDGKVFQCMFYALLGIPPLIM--JSLGERINTLVRYLLHRAK 144  
 DB 147 LFSFTLITTYGYGNVTPHQQCKVFLMIYGAFCIPPLI--ADLGRFSKAIAMALVQKYS 206  
 QY 145 KGLGMRADVSAN-----WVLGFESCISTLC--AAFSHYEH-WTFQAVIY 192  
 DB 207 KRELKQSDHEHLIREIAEVSPLYDLVLLVAGLF--VVFIA--AVIPLWENQLTYPDSYVF 264  
 QY 193 CETTLTIGFGDYVALOKDQALOTOPQYVAFSPVYITLC--VIGAPL 239  
 DB 265 SYMSLTITGLGDIIVPRMDPLPT-----LIVITTC--ITVALV 303

Search completed: August 28, 2001, 17:07:06  
 Job time: 475 sec



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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 28, 2001, 17:13:14 ; Search time 21.03 Seconds

(without alignments)  
641.781 Million cell updates/sec

Title: US-09-503-089a-5

Sequence: 1 MKRQNVRLALIVCTFTYLL.....STGLHSLSTFRGLMKRRSSV 394

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	204.2	100.0	394	1	C1W3_HUMAN
2	1850.5	90.6	411	1	C1W3_RAT
3	1840.5	90.1	409	1	C1W3_MOUSE
4	370	18.1	411	1	C1W2_MOUSE
5	364	17.8	426	1	C1W2_HUMAN
6	329.5	16.1	393	1	C1W4_HUMAN
7	326.5	16.0	398	1	C1W4_MOUSE
8	320.5	15.7	336	1	C1W1_HUMAN
9	319	15.6	499	1	C1W5_HUMAN
10	318.5	15.6	336	1	C1W1_MOUSE
11	295.5	14.5	313	1	C1W6_HUMAN
12	261.5	12.8	1001	1	ORL1_MOUSE
13	259.5	12.7	335	1	TRK8_MOUSE
14	224	11.0	307	1	C1W7_HUMAN
15	221	10.8	307	1	C1W8_MOUSE
16	170	8.3	691	1	TRK1_MOUSE
17	112.5	5.5	490	1	C1K1_MOUSE
18	99.5	4.9	1174	1	C1K1_MOUSE
19	98	4.8	1743	1	TAGC_MOUSE
20	97.5	4.8	228	1	TRK1_MOUSE
21	97.5	4.8	432	1	TRK1_MOUSE
22	96.5	4.7	449	1	TRK1_MOUSE
23	94.5	4.6	209	1	TRK1_MOUSE
24	94.5	4.6	385	1	TRK1_MOUSE
25	94.5	4.6	449	1	TRK1_MOUSE
26	94.5	4.6	647	1	TRK1_MOUSE
27	94	4.6	262	1	TRK1_MOUSE
28	94	4.6	287	1	TRK1_MOUSE
29	94	4.6	1159	1	TRK1_MOUSE
30	93.5	4.6	285	1	TRK1_MOUSE
31	93	4.6	529	1	TRK1_MOUSE
32	93	4.6	602	1	TRK1_MOUSE
33	92.5	4.5	653	1	TRK1_MOUSE

34	92.5	4.5	655	1	C1K4_RAT	P1585 ratu norv
35	92	4.5	451	1	IFR1_HUMAN	O00458 homo sapien
36	92	4.5	598	1	C1K5_RABIT	P00638 oryctolagus
37	91.5	4.5	660	1	C1K4_BOVIN	O05037 bos taurus
38	91.5	4.5	1581	1	WGLP-BEV	P23052 bovine vitru
39	91	4.5	601	1	C1K5_MOUSE	P79197 bovine vitru
40	90.5	4.4	290	1	LEP4_PSEAE	P22610 pseudomonas
41	90.5	4.4	369	1	PAR3_MOUSE	O08675 mus musculu
42	90.5	4.4	509	1	GTR4_HUMAN	P14672 homo sapien
43	90.5	4.4	654	1	C1K4_MOUSE	O28527 mustela put
44	90	4.4	393	1	TRK9_HUMAN	O28806 homo sapien
45	90	4.4	499	1	C1K2_HUMAN	P16389 homo sapien

## ALIGNMENTS

RESULT	ID	SEQUENCE	STANDARD	PRT	394 AA
1	C1W3_HUMAN	014649			
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9	C1W3_HUMAN	014649			
10	C1W3_HUMAN	014649			
11	C1W3_HUMAN	014649			
12	C1W3_HUMAN	014649			
13	C1W3_HUMAN	014649			
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42	C1W3_HUMAN	014649			
43	C1W3_HUMAN	014649			
44	C1W3_HUMAN	014649			
45	C1W3_HUMAN	014649			

DR InterPro: IPR003280; -.  
 DR Pfam: PF02034; TWIK\_channel; 1.  
 DR PRINTS: PR01095; TASKCHANNEL.  
 DR PRINTS: PR01333; 2PORKCHANNEL.  
 KM Ionic channel; Transmembrane; Ion transport; Potassium transport;  
 KW Glycoprotein.  
 FT DOMAIN 1 8 CYTOPLASMIC (POTENTIAL).  
 FT TRANSSEM 9 29 POTENTIAL.  
 FT DOMAIN 78 101 PORE-FORMING (POTENTIAL).  
 FT TRANSSEM 108 128 POTENTIAL.  
 FT DOMAIN 129 158 CYTOPLASMIC (POTENTIAL).  
 FT TRANSSEM 159 179 POTENTIAL.  
 FT DOMAIN 184 207 PORE-FORMING (POTENTIAL).  
 FT TRANSSEM 223 243 POTENTIAL.  
 FT DOMAIN 244 394 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 53 53 N-LINKED (GLCNAC...) (POTENTIAL).  
 SQ SEQUENCE 394 AA; 43518 MW; 9F94C8266F615FB7 CRC64;

Query Match 100.0%; Score 2042; DB 1; Length 394;  
 Best Local Similarity 100.0%; Pred. No. 7, 3e-156;  
 Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKRONVRLALIVCTFTYLLVGAAPDASEPELIERQLELRQELRARNLSGGGYE 60  
 1 MKRONVRLALIVCTFTYLLVGAAPDASEPELIERQLELRQELRARNLSGGGYE 60  
 DB 1 MKRONVRLALIVCTFTYLLVGAAPDASEPELIERQLELRQELRARNLSGGGYE 60  
 QY 61 ELEENVRLRPHKAGVOMRFGSFYFAITVTTTGYGHAAPSTGKVFCEVALLGIP 120  
 61 ELEENVRLRPHKAGVOMRFGSFYFAITVTTTGYGHAAPSTGKVFCEVALLGIP 120  
 DB 61 ELEENVRLRPHKAGVOMRFGSFYFAITVTTTGYGHAAPSTGKVFCEVALLGIP 120  
 QY 121 TLVWFSIGERINTLVRYLLHRAKKGIGMRADYSMANMVLIGFSCISTLCIGAAAF 180  
 121 TLVWFSIGERINTLVRYLLHRAKKGIGMRADYSMANMVLIGFSCISTLCIGAAAF 180  
 DB 121 TLVWFSIGERINTLVRYLLHRAKKGIGMRADYSMANMVLIGFSCISTLCIGAAAF 180  
 QY 121 TLVWFSIGERINTLVRYLLHRAKKGIGMRADYSMANMVLIGFSCISTLCIGAAAF 180  
 121 TLVWFSIGERINTLVRYLLHRAKKGIGMRADYSMANMVLIGFSCISTLCIGAAAF 180  
 DB 121 TLVWFSIGERINTLVRYLLHRAKKGIGMRADYSMANMVLIGFSCISTLCIGAAAF 180  
 QY 181 YEHTFFQAYYYCITLTITGFGDYVALQDQALQTOPQVYASFVYILGLTVIGAF 240  
 181 YEHTFFQAYYYCITLTITGFGDYVALQDQALQTOPQVYASFVYILGLTVIGAF 240  
 DB 181 YEHTFFQAYYYCITLTITGFGDYVALQDQALQTOPQVYASFVYILGLTVIGAF 240  
 QY 241 LVVLRFTMAEDKRAEHRALLTRNGQAGGGGSAHTTDTASSTAAGGGGFRVY 300  
 241 LVVLRFTMAEDKRAEHRALLTRNGQAGGGGSAHTTDTASSTAAGGGGFRVY 300  
 DB 241 LVVLRFTMAEDKRAEHRALLTRNGQAGGGGSAHTTDTASSTAAGGGGFRVY 300  
 QY 301 AEVLHFSQMSCLMYKSKREKLQYSIPMIIPRLSDTCEQSHSSPGGGGYSDFPSR 360  
 301 AEVLHFSQMSCLMYKSKREKLQYSIPMIIPRLSDTCEQSHSSPGGGGYSDFPSR 360  
 DB 301 AEVLHFSQMSCLMYKSKREKLQYSIPMIIPRLSDTCEQSHSSPGGGGYSDFPSR 360  
 QY 361 CLCGAPRSALSSYSTGLHSLSTFRGLMKRRSSV 394  
 361 CLCGAPRSALSSYSTGLHSLSTFRGLMKRRSSV 394  
 DB 361 CLCGAPRSALSSYSTGLHSLSTFRGLMKRRSSV 394

RESULT 2  
 C1W3\_RAT STANDARD; PRT; 411 AA.  
 AC 054912;  
 DT 01-OCT-2000 (Rel. 40, Created)  
 DT 01-OCT-2000 (Rel. 40, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE POTASSIUM CHANNEL SUBFAMILY K MEMBER 3 (ACID-SENSITIVE POTASSIUM CHANNEL PROTEIN TASK) (TWIK-RELATED ACID-SENSITIVE K+ CHANNEL).  
 GN KNCX3 OR TASK.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclerogasthi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID-10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Cerebellum;  
 RX MEDLINE=8099797; Pubmed=9437008;  
 RA Leonoudakis D., Gray A.T., Winegar B.D., Kindler C.H., Harada M., Taylor D.M., Chavez R.A., Forsythe J.R., Yost C.S.;  
 RT "An open rectifier potassium channel with two pore domains in tandem

RT cloned from rat cerebellum.";  
 RL J. Neurosci. 18:868-877(1998).  
 CC -1- FUNCTION: PH-DEPENDENT, VOLTAGE-INSENSITIVE, BACKGROUND POTASSIUM CHANNEL PROTEIN. RECTIFICATION DIRECTION RESULTS FROM POTASSIUM ION CONCENTRATION ON EITHER SIDE OF THE MEMBRANE. ACTS AS AN OUTWARD RECTIFIER WHEN EXTERNAL POTASSIUM CONCENTRATION IS LOW, WHEN EXTERNAL POTASSIUM CONCENTRATION IS HIGH, CURRENT IS INWARD (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL). EXPRESSION IN LUNG AND BRAIN. LOW LEVELS IN LIVER, KIDNEY AND SKELETAL MUSCLE.  
 CC -1- MISCELLANEOUS: INHIBITED BY EXTRACELLULAR ACIDIFICATION, ZINC, BUPIVACAINE AND PHENYTOIN. ACTIVATED BY PROTEIN KINASE A.  
 CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM CHANNELS.  
 CC -----  
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 CC -----  
 CC EMBL: AF031384; AAC39952.1; -.  
 DR InterPro: IPR000099; -.  
 DR InterPro: IPR001622; -.  
 DR InterPro: IPR003092; -.  
 DR InterPro: IPR003280; -.  
 DR Pfam: PF02034; TWIK\_channel; 1.  
 DR PRINTS: PR01095; TASKCHANNEL.  
 DR PRINTS: PR01333; 2PORKCHANNEL.  
 KM Ionic channel; Transmembrane; Ion transport; Potassium transport;  
 KW Glycoprotein.  
 FT DOMAIN 1 8 CYTOPLASMIC (POTENTIAL).  
 FT TRANSSEM 9 29 POTENTIAL.  
 FT DOMAIN 78 101 PORE-FORMING (POTENTIAL).  
 FT TRANSSEM 108 128 POTENTIAL.  
 FT DOMAIN 129 158 CYTOPLASMIC (POTENTIAL).  
 FT TRANSSEM 159 179 POTENTIAL.  
 FT DOMAIN 184 207 PORE-FORMING (POTENTIAL).  
 FT TRANSSEM 223 243 POTENTIAL.  
 FT DOMAIN 244 411 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 53 53 N-LINKED (GLCNAC...) (POTENTIAL).  
 SQ SEQUENCE 411 AA; 45276 MW; D2778016E09E215D CRC64;

Query Match 90.6%; Score 1850.5; DB 1; Length 411;  
 Best Local Similarity 88.3%; Pred. No. 1, 5e-140;  
 Matches 363; Conservative 8; Mismatches 2; Indels 17; Gaps 2;

QY 1 MKRONVRLALIVCTFTYLLVGAAPDASEPELIERQLELRQELRARNLSGGGYE 60  
 1 MKRONVRLALIVCTFTYLLVGAAPDASEPELIERQLELRQELRARNLSGGGYE 60  
 DB 1 MKRONVRLALIVCTFTYLLVGAAPDASEPELIERQLELRQELRARNLSGGGYE 60  
 QY 61 ELEENVRLRPHKAGVOMRFGSFYFAITVTTTGYGHAAPSTGKVFCEVALLGIP 120  
 61 ELEENVRLRPHKAGVOMRFGSFYFAITVTTTGYGHAAPSTGKVFCEVALLGIP 120  
 DB 61 ELEENVRLRPHKAGVOMRFGSFYFAITVTTTGYGHAAPSTGKVFCEVALLGIP 120  
 QY 121 TLVWFSIGERINTLVRYLLHRAKKGIGMRADYSMANMVLIGFSCISTLCIGAAAF 180  
 121 TLVWFSIGERINTLVRYLLHRAKKGIGMRADYSMANMVLIGFSCISTLCIGAAAF 180  
 DB 121 TLVWFSIGERINTLVRYLLHRAKKGIGMRADYSMANMVLIGFSCISTLCIGAAAF 180  
 QY 121 TLVWFSIGERINTLVRYLLHRAKKGIGMRADYSMANMVLIGFSCISTLCIGAAAF 180  
 121 TLVWFSIGERINTLVRYLLHRAKKGIGMRADYSMANMVLIGFSCISTLCIGAAAF 180  
 DB 121 TLVWFSIGERINTLVRYLLHRAKKGIGMRADYSMANMVLIGFSCISTLCIGAAAF 180  
 QY 181 YEHTFFQAYYYCITLTITGFGDYVALQDQALQTOPQVYASFVYILGLTVIGAF 240  
 181 YEHTFFQAYYYCITLTITGFGDYVALQDQALQTOPQVYASFVYILGLTVIGAF 240  
 DB 181 YEHTFFQAYYYCITLTITGFGDYVALQDQALQTOPQVYASFVYILGLTVIGAF 240  
 QY 241 LVVLRFTMAEDKRAEHRALLTRNGQAGGGGSAHTTDTASSTAAGGGGFRVY 300  
 241 LVVLRFTMAEDKRAEHRALLTRNGQAGGGGSAHTTDTASSTAAGGGGFRVY 300  
 DB 241 LVVLRFTMAEDKRAEHRALLTRNGQAGGGGSAHTTDTASSTAAGGGGFRVY 300  
 QY 292 -----GGGGRVNYAEVLHFSQMSCLMYKSKREKLQYSIPMIIPRLSDTCEQSHSSPGGGGYSDFPSR 343



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Db 301 GVGVGSGGGRNYAEMLFQSMCSCLMYKSKSEKIQYIPILIPDLSSTDCVSHS 360
Qy 344 HSPGGGGRYSDTPSRRLCSGAPRSATISSVSTGLHSLSTRGLMKRRSSV 394
    |||||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 361 HSPGGGGRYSDTPSRRLCSGAPRSATISSVSTGLHSLSTRGLMKRRSSV 411

RESULT 3
CIW3_MOUSE STANDARD: PRT: 409 AA.
AC 035111: 035163;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE POTASSIUM CHANNEL SUBFAMILY K MEMBER 3 (ACID-SENSITIVE POTASSIUM
CHANNEL PROTEIN TASK) (TWIK-RELATED ACID-SENSITIVE K+ CHANNEL)
DE (CARDIAC TWO-PORE BACKGROUND K+ CHANNEL) (CTBAK-1).
GN KCNK3 OR TASK OR CTBAK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RX MEDLINE=97459933; PubMed=9312005;
RA Duprat F., Lesage F., Fink M., Reyes R., Heurteaux C., Lazdunski M.;
RT "TASK, a human background K+ channel to sense external pH variations
near physiological pH."
RL EMBO J. 16:5464-5471(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20287574; PubMed=10748056;
RA Lopes C.M., Gallagher P.G., Buck M.E., Butler M.H., Goldstein S.A.;
RT "Proton block and voltage gating are potassium-dependent in the
cardiac leak channel hcnk3."
RL J. Biol. Chem. 275:16969-16978(2000).
CC -1- FUNCTION: PH-DEPENDENT VOLTAGE-INSENSITIVE, BACKGROUND POTASSIUM
CHANNEL PROTEIN. RECTIFICATION DIRECTION RESULTS FROM POTASSIUM
ION CONCENTRATION ON EITHER SIDE OF THE MEMBRANE. ACTS AS AN
OUTWARD RECTIFIER WHEN EXTERNAL POTASSIUM CONCENTRATION IS LOW.
WHEN EXTERNAL POTASSIUM CONCENTRATION IS HIGH, CURRENT IS INWARD
(BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- TISSUE SPECIFICITY: VERY STRONG EXPRESSION IN HEART, ALSO DETECTED
IN KIDNEY, BRAIN, SKIN, TESTIS, LUNG, SKELETAL MUSCLE, SMALL
INTESTINE AND STOMACH. NOT DETECTED IN LIVER, THYMUS OR SPLEEN.
CC -1- MISCELLANEOUS: INACTIVATED BY BARIUM.
CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
CHANNELS.
CC -----
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AB008537; BAA25436.1; -
DR EMBL: AF006824; AAC53367.1; -
DR EMBL: AB013345; BAA28349.1; -
DR EMBL: AF241798; AAF81418.1; -
DR EMBL: AF242508; AAF81418.1; JOINED.

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DR MGD; MG1:1100509; Kcnk3.
DR InterPro: IPR000099; -.
DR InterPro: IPR001622; -.
DR InterPro: IPR003092; -.
DR InterPro: IPR003280; -.
DR Pfam: PF02034; TWIK_channel; 1.
DR PRINTS: PRO1095; TASKCHANNEL.
DR PRINTS: PRO1333; 2PORECHANNEL.
KW Ionic channel; Transmembrane; Ion transport; Potassium transport;
KW Glycoprotein.
FT DOMAIN 1 8 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 9 29 POTENTIAL.
FT DOMAIN 78 101 PORE-FORMING (POTENTIAL).
FT TRANSMEM 108 128 POTENTIAL.
FT DOMAIN 129 158 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 159 179 POTENTIAL.
FT DOMAIN 184 207 PORE-FORMING (POTENTIAL).
FT TRANSMEM 223 243 POTENTIAL.
FT DOMAIN 244 409 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 53 53 N-LINKED (GLCN) (POTENTIAL).
FT CONFLICT 4 4 Q -> E (IM REF.).
FT CONFLICT 123 123 V -> I (IN REF.).
SQ SEQUENCE 409 AA; 45068 MW; 35236E011AAC; CRC64;

Query Match 90.1%; Score 1840.5; Length 409;
Best Local Similarity 88.5%; Pred. No. 9.2e-03;
Matches 362; Conservative 7; Mismatches 55; Indels 15; Gaps 2;

Qy 1 MKRONVRLALIVCTFTYLLVGAADFALAESEPELIERC VROELRARNYNSGGYE 60
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Db 1 MKRONVRLALIVCTFTYLLVGAADFALAESEPELIERC VROELRARNYNSGGYE 60
Qy 61 ELERVVLRLKPKKGVQWRFGSPFATVTTTGYGA STGGKVCMEFVALIGPL 120
    |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 61 ELERVVLRLKPKKGVQWRFGSPFATVTTTGYGA STGGKVCMEFVALIGPL 120
Qy 121 TLVNFOSIGERINTLVRLHRAKGLGMRADYSMANV TGFESCISTICIGNAFSH 180
    |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 121 TLVNFOSIGERINTLVRLHRAKGLGMRADYSMANV TGFESCISTICIGNAFSH 180
Qy 181 YEHWFQAYYYCFTLTGTPGIDVALQKQADOTQCF VSFVYLTGLVYIGAFIN 240
    |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 181 YEHWFQAYYYCFTLTGTPGIDVALQKQADOTQCF VSFVYLTGLVYIGAFIN 240
Qy 241 LVVLRFTMNMDERKRDHRAALLTRNGOAGGGGSGSATTTTASTTAA- 291
    |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 241 LVVLRFTMNMDERKRDHRAALLTRNGOAGGGGSGSATTTTASTTAA- 291
Qy 292 -----GGGGRNYAEEVLHFQSMCSCLMYKSKRELOV VITPRDLSSTDCVSHS 345
    |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 292 -----GGGGRNYAEEVLHFQSMCSCLMYKSKRELOV VITPRDLSSTDCVSHS 345
Qy 346 SPGGGGRYSDTPSRRLCSGAPRSATISSVSTGLHSLSTRGLMKRRSSV 394
    |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 346 SPGGGGRYSDTPSRRLCSGAPRSATISSVSTGLHSLSTRGLMKRRSSV 394
Qy 361 SPGGGGRYSDTPSRRLCSGAPRSATISSVSTGLHSLSTRGLMKRRSSV 409
    |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 361 SPGGGGRYSDTPSRRLCSGAPRSATISSVSTGLHSLSTRGLMKRRSSV 409

RESULT 4
CIW2_MOUSE STANDARD: PRT: 411 AA.
AC P97438;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE POTASSIUM CHANNEL SUBFAMILY K MEMBER 2 (OUTWARD RECTIFYING POTASSIUM
CHANNEL PROTEIN TASK) (TWIK-RELATED ACID-SENSITIVE K+ CHANNEL)
DE (CARDIAC TWO-PORE BACKGROUND K+ CHANNEL) (CTBAK-1).
GN KCNK2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;

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RP [1] SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
RN
RC TISSUE-Brain;
RX MEDLINE-97157476; PubMed-9003761;
RA Fink M., Duprat F., Lesage F., Reyes R., Romey G., Heurteaux C.,
  Lazdunski M.;
RT "Cloning, functional expression and brain localization of a novel
  unconventional outward rectifier K+ channel.";
RN EMBL J. 15:6854-6862(1996).
RP
RC REVISIONS.
RC TISSUE-Brain;
RA Fink M., Duprat F., Lesage F., Reyes R., Romey G., Heurteaux C.,
  Lazdunski M.;
RN Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RP
RC ACTIVATION.
RC MEDLINE-99254548; PubMed-10321245;
RA Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.;
RT "Inhalational anesthetics activate two-pore-domain background K+
  channels.";
RN Nat. Neurosci. 2:422-426(1999).
RP
RC -1- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL.
RC -1- SUBUNIT: HOMODIMER (POTENTIAL).
RC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- TISSUE SPECIFICITY: HIGH EXPRESSION IN BRAIN AND LUNG. ALSO
CC DETECTED IN KIDNEY, HEART AND SKELETAL MUSCLE. NOT DETECTED IN
CC LIVER. IN THE BRAIN, HIGHEST EXPRESSION IN OLFACTORY BULB,
CC HIPPOCAMPUS AND CEREBELLUM.
CC -1- MISCELLANEOUS: INHIBITED BY BARIUM. ACTIVATED BY VOLATILE GENERAL
CC ANAESTHETICS SUCH AS CHLOROFORM, DIETHYL ETHER, HALOTHANE AND
CC ISOFLURANE.
CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
CC CHANNELS.
CC
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL: U73488; AAC53005.2; -.
CC DR MGD; MG1:109366; KCMK2.
CC DR InterPro: IPR000099; -.
CC DR InterPro: IPR001622; -.
CC DR InterPro: IPR003280; -.
CC DR Pfam: PFO02034; TWIK.channel; 1.
CC DR PRINTS: PRO1333; 2PORECHANNEL.
CC KW Ionic channel; Transmembrane; Ion transport; Potassium transport;
CC Glycoprotein.
CC FT DOMAIN 1 46 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 47 67 PORE-FORMING (POTENTIAL).
CC FT DOMAIN 129 155 PORE-FORMING (POTENTIAL).
CC FT TRANSMEM 157 177 CYTOPLASMIC (POTENTIAL).
CC FT DOMAIN 178 207 PORE-FORMING (POTENTIAL).
CC FT TRANSMEM 208 228 PORE-FORMING (POTENTIAL).
CC FT DOMAIN 238 268 PORE-FORMING (POTENTIAL).
CC FT TRANSMEM 273 293 CYTOPLASMIC (POTENTIAL).
CC FT DOMAIN 294 411 ESSENTIAL FOR CHLOROFORM AND HALOTHANE
CC FT DOMAIN 378 411 SENSITIVITY.
CC FT DOMAIN 354 411 REQUIRED FOR BASAL CHANNEL ACTIVITY.
CC FT CARBOHYD 95 95 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SO SEQUENCE 411 AA; 45297 MW; 8F97DD6D103EFA05 CRC64;
CC
CC Query Match 18.18; Score 370; DB 1; Length 411;
CC Best Local Similarity 28.08; Pred. No. 2.le-22;
CC Matches 109; Conservative 66; Mismatches 126; Indels 88; Gaps 13;

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Cc      1 MKRQVRLTLALICVFTLLVGAANFADLLESPELIER. 100ELRLARVNLSSGGYE 60
Cc      42 MKMKVSTIFLTV--VLTLIGAAVFAKLEOPDELISQRT. 100KQTFIAQACVNS--T 97
Cc      61 ELERVVLTL-KPKHKGV-----QMRAGSEFYVA. 100TIGYGAAPSTDGKV 108
Cc      98 ELDELIGQIVAAINNGIILPLGNSSNOVSHMDGSSFFV. 100TITGGINISPRREGGI 157
Cc      109 FCMFYALLGIPLTLVMEFOSLGERINTLVRYLHLRAKKGI. 100KAD-----VSM 156
Cc      158 FCLIIALLGILPLFGFLTAGVGDQLGTIF-----CK. 100VEDTFIKMNVSOTKIRI 208
Cc      157 ANMVLIGFESCITSLICIAAASFHEHMTFPQAYYYCF. 100FGFGVVALOKQKALOT 216
Cc      209 ISTIFILFGCVLFPALPAVLVIFKHLIEGSSALDAIFVYI. 100FGFGDVAGGSD--LEY 266
Cc      217 QPQYVAFSEFVYLTFLTYIGAFNLV--VLREPMINAEI. 100ADGHRALLFRNGAGGAG 274
Cc      267 LDFYFVWVWMLTVLALFAVLAIVLSIGMLKRVISKTKV. 100----- 307
Cc      275 GGGSAHTTDTGASTTAAGGCGFRNYAEVLHQSMSCLVYSKREKLOYSLPMLIPRDL 334
Cc      -308 GEFRAHAAEMTA-----NVTAE-----FKETRRRLSVEI-----YDKF 340
Cc      335 TSDTCEVQSHSPGGGGGRYSD--TPSRRL 362
Cc      341 QRATSVKRRLLSELAGNHNDELTPCRRLL 369
Cc
Cc      RESULT 5
Cc      C1W2_HUMAN STANDARD: PRT: 426 AA
Cc      AC 095069; Q9UNE3;
Cc      DT 01-OCT-2000 (Rel. 40, Created)
Cc      DT 01-OCT-2000 (Rel. 40, Last sequence update)
Cc      DT 01-OCT-2000 (Rel. 40, Last annotation update)
Cc      DE POTASSIUM CHANNEL SUBFAMILY K MEMBER 2 (OUTWARD RECTIFYING POTASSIUM
Cc      CHANNEL PROTEIN TREK-1) (TWO-PORE POTASSIUM CHANNEL TPCK1) (TREK-1 K+
Cc      CHANNEL SUBUNIT).
Cc      DE CNCK2 OR TREK.
Cc      GN Homo sapiens (Human).
Cc      OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Cc      CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Cc      OX NCBI_TaxId=9606;
Cc      RN [1]
Cc      RP SEQUENCE FROM N.A.
Cc      RX MEDLINE=99254548; PubMed=10321245;
Cc      RA Patel A.J., Honore E., Lesage F., Fink M., Boy G., Lazdunski M.,
Cc      RT "Inhalational anesthetics activate two-pore K+ main background K+
Cc      RL channels."
Cc      RL Nat. Neurosci. 2:422-426(1999).
Cc      RN [2]
Cc      RP SEQUENCE FROM N.A.
Cc      RC TISSUE-Brain;
Cc      RA Price L.A., Hellings S.E., Hayashi J.H., Patch M.H.;
Cc      Submitted (MAY-1997) to the EMBL/GenBank/DC databases.
Cc      -1- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL.
Cc      -1- SUBUNIT: HOMODIMER (POTENTIAL).
Cc      -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
Cc      -1- MISCELLANEOUS: ACTIVATED BY VOLATILE GENEAL ANAESTHETICS SUCH AS
Cc      CHLOROFORM, HALOTHANE AND ISOFURANE.
Cc      -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
Cc      CHANNELS.
Cc
Cc      -----
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Cc      or send an email to license@isb-sib.ch).
Cc
Cc      EMBL; AF129399; AA047569.1; -

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DB 235 VWFMLGLAFVASYLTIGNMLRVSSRR-----TRAENGILTAQA 275  
 QY 277 GSAHTDTFASSTAAG 292  
 DB 276 ASWTGTIVTARVORAG 291

RESULT 7  
 ID C1M4\_MOUSE STANDARD: PRT: 398 AA.  
 AC 088454; 01-OCT-2000 (Rel. 40, Created).  
 DT 01-OCT-2000 (Rel. 40, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE POTASSIUM CHANNEL SUBFAMILY K MEMBER 4 (TWIK-RELATED ARACHIDONIC ACID-STIMULATED POTASSIUM CHANNEL PROTEIN) (TRAAK).  
 GN KCNK4 OR TRAAK.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=98292450; PubMed=9628867;  
 RA Fink M., Lesage F., Duprat F., Heurteaux C., Reyes R., Fosset M., Lazdunski M.;  
 RT "A neuronal two P domain K+ channel stimulated by arachidonic acid and polyunsaturated fatty acids.";  
 RL EMBO J. 17:3297-3308(1998).  
 RN [2]  
 RP ACTIVATION.  
 RX MEDLINE=99254548; PubMed=10321245;  
 RA Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.;  
 RT "Inhalational anesthetics activate two-pore-domain background K+ channels.";  
 RL Nat. Neurosci. 2:422-426(1999).  
 CC -1- FUNCTION: VOLTAGE INSENSITIVE, INSTANTANEOUS, OUTWARDLY RECTIFYING POTASSIUM CHANNEL. OUTWARD RECTIFICATION IS REVERSED AT HIGH EXTERNAL K+ CONCENTRATIONS.  
 CC -1- SUBUNIT: HOMODIMER (POTENTIAL).  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2/TRAAT/TRUNCATED; ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, SPINAL CORD AND EYE. NOT DETECTED IN HEART, SKELETAL MUSCLE, LIVER, LUNGS, KIDNEY AND TESTIS.  
 CC -1- MISCELLANEOUS: ACTIVATED BY ARACHIDONIC ACID AND OTHER UNSATURATED FATTY ACIDS. NOT AFFECTED BY VOLATILE GENERAL ANESTHETICS SUCH AS CHLOROFORM, DIETHYL ETHER, HALOTHANE AND ISOFLURANE.  
 CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM CHANNELS.  
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 CC -----  
 CC EMBL: AF056492; AAC40181.1; -  
 DR MGD: MGI:1298234; KCNK4.  
 DR InterPro: IPR000099; -  
 DR InterPro: IPR001622; -  
 DR InterPro: IPR003280; -  
 DR Pfam: PF02034; TWIK channel. 1.  
 DR PRINTS: PR01333; 2PORECHANEL.  
 KM Ionic channel; Transmembrane; Ion transport; Potassium transport; Glycoprotein; Alternative splicing.  
 FT DOMAIN 1 3 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 4 24 POTENTIAL.  
 FT DOMAIN 89 113 PORE-FORMING (POTENTIAL).  
 FT

FT TRANSMEM 119 139 POTENTIAL.  
 FT DOMAIN 140 171 CYTOPLASMIC (PC, EMTIAL).  
 FT TRANSMEM 172 192 POTENTIAL.  
 FT DOMAIN 198 222 PORE-FORMING (POTENTIAL).  
 FT TRANSMEM 235 255 POTENTIAL.  
 FT DOMAIN 256 298 POTENTIAL.  
 FT CARBOHYD 81 81 N-LINKED (GLCN... ) (POTENTIAL).  
 FT CARBOHYD 84 84 N-LINKED (GLCN... ) (POTENTIAL).  
 FT VARSPLIC 63 67 KLIVE -> KAMAI (IN ISOFORM 2).  
 FT VARSPLIC 68 398 MISSING (IN ISOFORM 2).  
 SQ SEQUENCE 398 AA; 43051 MW; 4784834B7B7AFC3 CRC64.

Query Match 16.0%; Score 326.5; Ls: Length 398;  
 Best Local Similarity 31.5%; Pred. No. 6; Ls: 1;  
 Matches 85; Conservative 45; Mismatches 5; Indels 45; Gaps 7;

QY 9 LALIVCTFTYLLVGAANVPALESEPELIERORLET-ROK VARRNLSGGYEELERVL 67  
 DB 7 LALLALVLLVLYSGALVPALEPHEQQAOKKMDHGRDQ VDHPCVSKSLEDFFKLLV 66  
 QY 68 RLKPKAGVQ-----WRPAGSYFAIVYTTT VAAAPSTCGKVFCCFFYL 115  
 DB 67 EALGGGANPETSMTNNSNHSAMNLSAFAFFSGTITTT VNYLHTDAGRIFCIFYAL 126  
 QY 116 LGIPLTVMFOSIGERINTLVRLYLRARAKGLGMRA-----DVSANMVL 162  
 DB 127 VGIPFLGMLLAGVDRGLSGSLR-----RGIGHIETAT VAVPGLVRSLSAVFLFI 179  
 QY 163 GFSCISTLCIGAAAFSHYEHMTFFOAYVYCTTTTGFVVALOKDALQTOPQV-- 220  
 DB 180 G---CLLFVLPTFPVFSVSWMSKLEAIFYVITLVGVF TRVV--PGDGTGQNSPAYOP 234  
 QY 221 -----VAFSEVILIGLTYIGAFINLVYLR 245  
 DB 235 LVWFMLGLAFVASYLTIGNMLRVSSRR 264

RESULT 8  
 ID C1M4\_HUMAN STANDARD: PRT: 336 AA.  
 AC 000180; Q13307;  
 DT 01-OCT-2000 (Rel. 40, Created)  
 DT 01-OCT-2000 (Rel. 40, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE POTASSIUM CHANNEL SUBFAMILY K MEMBER 1 (INWARDLY RECTIFYING POTASSIUM CHANNEL PROTEIN TWIK-1) (POTASSIUM CHANNEL K.3.1.1).  
 GN KCNK1 OR TWIK1 OR HOH01 OR KCNO1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A., FUNCTION, AND MUTAGENESIS OF THR-161.  
 RC TISSUE=Kidney;  
 RX MEDLINE=96183184; PubMed=8605869;  
 RA Lesage F., Guillemare E., Fink M., Duprat F., Lazdunski M., Romey G., Barhanin J.;  
 RT "TWIK-1, a ubiquitous human weakly inward rectifying K+ channel with a novel structure.";  
 RL EMBO J. 15:1004-1011(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A., AND REVIEW.  
 RC TISSUE=Brain;  
 RX MEDLINE=98122696; PubMed=9462864;  
 RA Goldstein S.A.N., Wang K.-W., Ilan N., Pausch M.H.;  
 RT "Sequence and function of the two P domain potassium channels: implications of an emerging superfamily.";  
 RL J. Mol. Med. 76:13-20(1998).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Desir G.V., Orlas M., Freeman T.;  
 RT Submitted (Apr-1997) to the EMBL/Genbank/DBJ databases.

```

CC -1- FUNCTION: WEAKLY INWARD RECTIFYING POTASSIUM CHANNEL.
CC -1- SUBUNIT: HOMODIMER (POTENTIAL).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGH LEVELS IN HEART AND BRAIN AND LOWER LEVELS IN PLACENTA, LUNG, LIVER AND KIDNEY.
CC -1- MISCELLANEOUS: INHIBITED BY BARIUM, QUININE, QUINIDINE AND INTERNAL ACIDIFICATION. ACTIVATED BY PROTEIN KINASE C.
CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM CHANNELS.
CC -----
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CC -----
CC DR EMBL: U33632; AAB01688.1; -
CC DR EMBL: U76996; AAB97878.1; -
CC DR EMBL: U90065; AAB51147.1; -
CC DR MIM: 601745; -
CC DR InterPro: IPR000099; -
CC DR InterPro: IPR001622; -
CC DR InterPro: IPR001779; -
CC DR InterPro: IPR003280; -
CC DR Pfam: PF02034; TWIK-channel; 1.
CC DR PRINTS: PRO1096; TWIKCHANNEL.
CC DR PRINTS: PRO1333; 2PORECHANNEL.
CC KM Ionic channel; Transmembrane; Ion transport; Potassium transport; Glycoprotein.
CC FT DOMAIN 1 20 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 21 41 POTENTIAL.
CC FT DOMAIN 104 130 PORE-FORMING (POTENTIAL).
CC FT TRANSMEM 133 153 POTENTIAL.
CC FT DOMAIN 154 177 CYTOPLASMIC (POTENTIAL).
CC FT TRANSEM 178 198 POTENTIAL.
CC FT DOMAIN 212 238 PORE-FORMING (POTENTIAL).
CC FT TRANSEM 247 267 POTENTIAL.
CC FT DOMAIN 268 336 CYTOPLASMIC (POTENTIAL).
CC FT CARBOHYD 95 95 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT MUTAGEN 161 161 T-2A: NO EFFECT ON CHANNEL ACTIVITY.
CC SQ SEQUENCE 336 AA; 38143 MW; 244ID950132321SD CRC64;
Query Match 15.7%; Score 320.5; DB 1; Length 336;
Best Local Similarity 32.4%; Pred. No. 1.5e-18;
Matches 90; Conservative 47; Mismatches 102; Indels 39; Gaps 9;
OY 11 LIVCTFTYLLVGAADFALDESEPELIERQRL-ELRQDELARARYNLSSGVELELERVLR 69
OY 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11:
Db 26 LVLDGYLLYLVGAVAVSSVELPYEDLLRQELRLKRLRFLREHECHESQQLRQFLGRVLEA 85
OY 70 KPRKAGV-----QRRFAGSFYFAIVYITTTIGGAAPSTDSGKVCYCMFYALGIPLT 121
OY 86 SNYGVSYSNAGSNGMWMDFTSALFFASTVLSITGSGHVPVLSDGKACFCIIYSVIGIPFT 145
OY 122 LVMEQSLGERINTLVRLYLHRAKKGL-----GMRADVSAMNANVLLGFPSCISLTIG 174
Db 146 LLEFLTAVQRIT-----VHTRRVLVLFHIRWGSKOVVAIVAVHVLGLGFTVSCFEPTP 199
OY 175 AAASFHVE-HMTFQAVYYFCITLTITIGGDYVA-----LQDQDALOTOPQYVAFSFYIL 229
OY 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11:
Db 200 AAVFSVLEDDNNPLFESFECFISLSTIGLDGYVPEGVGNQKFRLE-----YKIGITCYLL 254
OY 230 TG----LTVIGAFNLNVL---RRFTNAADEKRDRAEH 260
OY 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11:
Db 255 LGLTAMLVLETFCLELHKLKFRKMFYVKKDKDKEDQVH 292

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AC 095279: 2000 (Rel. 40, Created)
DT 01-Oct-2000 (Rel. 40, Last sequence update)
DT 01-Oct-2000 (Rel. 40, Last annotation update)
DE POTASSIUM CHANNEL SUBFAMILY K MEMBER 5 (ACLI, SENSITIVE POTASSIUM
DE CHANNEL PROTEIN TASK-2) (TWIK-RELATED ACID-FUNCTION FIVE K+ CHANNEL 2).
GN KCNK5 OR TASK2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
ON NCBI_Taxid=9606;
RX MEDLINE=99030343; PubMed=8812978;
RA Reyes R., Duprat F., Lesage F., Fink M., Sejerling A.M., Farman N.,
RA Lazdunski M.;
RT "Cloning and expression of a novel pH-sensitive two pore domain K+
channel from human kidney";
RL J. Biol. Chem. 273:30863-30869(1998).
CC -!- FUNCTION: PH DEPENDENT, VOLTAGE INSENSITIVE. OUTWARDLY RECTIFYING
CC POTASSIUM CHANNEL. OUTWARD RECTIFICATION LOST AT HIGH EXTERNAL
CC K+ CONCENTRATIONS.
CC -!- SUBUNIT: HOMODIMER (POTENTIAL).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -!- TISSUE SPECIFICITY: ABUNDANT EXPRESSION IN KIDNEY, ALSO DETECTED
CC IN LIVER, PLACENTA AND SMALL INTESTINE. IN THE KIDNEY, EXPRESSION
CC IS RESTRICTED TO THE DISTAL TUBULES AND COLLECTING DUCTS. NOT
CC EXPRESSED IN PROXIMAL TUBULES OR GLOMERULI.
CC -!- MISCELLANEOUS: INHIBITED BY QUININE, QUINIDINE AND EXTERNAL
CC ACIDIFICATION.
CC -!- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
CC CHANNELS.
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CC or sent an email to license@sib.ch)
CC -----
CC EMBL, AF084830; AAC79458.1; -.
DR MIR, 603493; -.
DR InterPro: IPR000099; -.
DR InterPro: IPR001622; -.
DR InterPro: IPR003280; -.
DR Pfam, PF02034; TWIK-channel; 1.
DR PRINTS: PR01333; 2PORECHANNEL.
KW Ionic channel; Transmembrane; Ion transport; Plasma membrane transport;
KW Glycoprotein.
KW DOMAIN 1 7 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 8 26 POTENTIAL.
FT DOMAIN 85 112 PORE-FORMING (POTENTIAL).
FT TRANSSEM 113 133 POTENTIAL.
FT DOMAIN 134 157 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 158 180 POTENTIAL.
FT DOMAIN 190 215 PORE-FORMING (POTENTIAL).
FT TRANSSEM 230 250 POTENTIAL.
FT DOMAIN 251 325 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 77 77 N-LINKED (GLYCOSYLATION) (POTENTIAL).
SQ SEQUENCE 499 AA; 55130 MW; B871A7AA8231 CRC64;
Query Match 15.6%; Score 319; Dr Length 499;
Best Local Similarity 32.8%; Pred. No. 3.1; Indels 28; Gaps 8;
Matches 84; Conservative 47; Mismatches 1;
OY 18 YLLGAQAVFDLSEPELT-----RRLLEHQDELRA--SGGYEELERV-----66
DB 15 YLAIGAAIFEVLE-EPHKKEAKNNYYTKLHL----LR--TLGGEGDKITLEVSDAG 69
DY 67 --LRLPKKAGVQMRFAGSFYAIVTTTGYGHAAP---KYVCMEYALLGIPLLTVM 124

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RN [2]  
 RP SEQUENCE FROM N.A., AND MUTAGENESIS OF CYS-53.  
 RC TISSUE-Brain;  
 RA MEDLINE-99175162; PubMed-10075682;  
 RA Chavez R.A., Gray A.T., Zhao B.B., Kindler C.H., Mazurek M.J.,  
 RT "TWIK-2, a new weak inward rectifying member of the tandem pore domain  
 potassium channel family."  
 RL J. Biol. Chem. 274:7887-7892(1999).  
 RN [3]  
 RP ERRATUM.  
 RA Chavez R.A., Gray A.T., Zhao B.B., Kindler C.H., Mazurek M.J.,  
 RL J. Biol. Chem. 274:24440-24440(1999).  
 CC -1- FUNCTION: WEAK INWARDLY RECTIFYING POTASSIUM CHANNEL.  
 CC -1- SUBUNIT: HOMODIMER (POTENTIAL).  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).  
 CC -1- TISSUE SPECIFICITY: WIDESPREAD EXPRESSION, DETECTED IN ALL TISSUES  
 TESTED EXCEPT FOR SKELETAL MUSCLE. STRONGEST EXPRESSION IN  
 PLACENTA, PANCREAS, HEART, COLON AND SPLEEN, LOWER LEVELS DETECTED  
 IN PERIPHERAL BLOOD LEUKOCYTES, LUNG, LIVER, KIDNEY AND THYMUS.  
 CC -1- LOWEST EXPRESSION DETECTED IN BRAIN.  
 CC -1- MISCELLANEOUS: INHIBITED BY INTERNAL ACIDIFICATION AND, TO A SMALL  
 DEGREE, BY ZINC. NOT INHIBITED BY QUININE, QUINIDONE OR BARIUM.  
 CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM  
 CHANNELS.  
 CC -----  
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 CC -----  
 DR EMBL: AF134149; AAD22980.1;  
 DR EMBL: AF117708; AAD24000.1;  
 DR MIM: 603939;  
 DR InterPro: IPR001622;  
 DR InterPro: IPR001779;  
 DR PRINTS: PR01096; TWIK1CHANNEL.  
 KW Ionic channel; Transmembrane; Ion transport; Potassium transport;  
 KW Glycoprotein.  
 FT DOMAIN 1 4 CYTOPLASMIC (POTENTIAL).  
 FT TRANSSEM 5 25 POTENTIAL.  
 FT DOMAIN 90 115 PORE-FORMING (POTENTIAL).  
 FT TRANSSEM 121 141 POTENTIAL.  
 FT DOMAIN 142 172 CYTOPLASMIC (POTENTIAL).  
 FT TRANSSEM 173 193 PORE-FORMING (POTENTIAL).  
 FT DOMAIN 199 223 PORE-FORMING (POTENTIAL).  
 FT TRANSSEM 236 256 POTENTIAL.  
 FT DOMAIN 257 313 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 79 79 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 85 85 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT MOTAGN 53 53 C->A: NO CHANNEL ACTIVITY.  
 FT MOTAGN 53 53 C->A: NO CHANNEL ACTIVITY.  
 SQ SEQUENCE 313 AA; 33747 MW; 1379382DFB0575DE CRC64;  
 Query Match 14.5%; Score 295.5; DB 1; Length 313;  
 Best Local Similarity 31.7%; Pred. No. 1,4e-16;  
 Matches 90; Conservative 40; Mismatches 95; Indels 59; Gaps 12;  
 Oy 18 YLVGAAVFDLSEPELIERORLEKROELRARN-----LSGGYELE 63  
 Db 17 YLVGALLVRLLESPHARLRAELLETIRALQLQSPCAAPALAPFERYVLAAG---RLG 73  
 Oy 64 RVLRLKPKHAGVQ---WRPAGSFYATVTTTGYGHAPESTDGKVCMFVALLGLPT 120  
 Db 74 RVLVLANSGSNASDPAMDPAFSAFLFASTLTITVGYGTPFLTDAGKAFSIAFALLGVP 133  
 Oy 121 TLVNFQSLGELINLVRLHLRAKKGIGM-----RADVSMAMNVLGIFSCSTLTC-- 172  
 Db 134 TMLLTASQRLSL---LTHVPLSWLSMRWGMDPRRA---ACMHLVALGIVVTVCF 186

Oy 173 IGAAAFSHYEH-WTFEPAAYYCITLTITIGFDYVALQF-VA-ATQPO---VVAESFYVI 228  
 Db 187 VPAVIFAHLEBAWSEFLDAFYCFISLTISLTIGDYVPGE---AVGQPYRALYKVLVTVYL 242  
 Oy 229 LTGLT-----VIGAFNLVYLRFM-----MR-DFKR 256  
 Db 243 FLGLVAMVLYQTRHVSDDLGLTELILPPCPASFP-----LDR 286  
 RESULT 12  
 ORK1\_DROME STANDARD; PRT: 1001 AA;  
 AC 094526;  
 DT 01-OCT-2000 (Rel. 40, Created)  
 DT 01-OCT-2000 (Rel. 40, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE OPEN RECTIFIER POTASSIUM CHANNEL PROTEIN 1, TWO PORE DOMAIN POTASSIUM  
 CHANNEL ORK1.  
 GN ORK1 OR CG1615.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_Taxid=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Larva;  
 RX MEDLINE-97075152; PubMed-8917578;  
 RA Goldstein S.A.N., Price L.A., Rosenthal D.N., Emsch M.H.,  
 RT "ORK1, a potassium-selective leak channel with two pore domains  
 cloned from Drosophila melanogaster by expression in Saccharomyces  
 cerevisiae."  
 RL Proc. Natl. Acad. Sci. U.S.A. 93:13256-13261(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BERKELEY;  
 RX MEDLINE-20196006; PubMed-10731132;  
 RA Adams M.D., Celiker S.E., Holt R.A., Evans J., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hosick R.A., Galie R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhao Z., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Cline M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nee C.R., Miklos G.L.G.,  
 RA Abell J.F., Agbayani A., An H.-J., Andrews S., Binkov C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandal D., Boltsakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brooks D., Brothier P.,  
 RA Burdick K.C., Busam D.A., Butler H., Cadieu C., Center A., Chandra I.,  
 RA Cherry J.M., Cavley S., Dahlke C., Davenport D., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.E., Weng L., Dietz S.M.,  
 RA Dodson K.J., Doup L.E., Downes M., Dugan-Rochet A., Dunkov B.G., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Fierman J., Fierman S., Fleischmann W.,  
 RA Foster C., Gabriellian A.E., Gary N.S., Gellera J.W., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gu Z., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei J.-H., Iobagwan C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Nelson J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M., Skerz M.P., Smith T.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris S., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Murray D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.M., Paclet J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Schenker F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skerz M.P., Smith T.,  
 RA Spier E.C., Spadling A.C., Stapleton M., Strickland S., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu J., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,







## CHANNELS.

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 CC -----

EMBL: AF110521; AAD29577.1; ALT\_TERM.

EMBL: AB015729; BA35074.1; -

EMBL: AF028220; AAD09337.1; -

EMBL: AF012324; AAF21603.1; -

EMBL: AF158234; AAF14528.1; -

MGI: 1341841; Kcnk8.

InterPro: IPR001622; -

InterPro: IPR003280; -

PRINTS: PRO1333; 2PORKCHANNEL.

Ionic channel; Transmembrane; Ion transport; Potassium transport;

Glycoprotein.

DOMAIN 1 10 CYTOPLASMIC (POTENTIAL).

TRANSMEM 11 31 POTENTIAL.

TRANSMEM 92 118 PORE-FORMING (POTENTIAL).

TRANSMEM 120 140 POTENTIAL.

TRANSMEM 141 172 CYTOPLASMIC (POTENTIAL).

TRANSMEM 173 193 POTENTIAL.

TRANSMEM 199 227 PORE-FORMING (POTENTIAL).

TRANSMEM 233 253 POTENTIAL.

DOMAIN 254 307 CYTOPLASMIC (POTENTIAL).

CARBOHYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).

CONFLICT 1 3 MGS -> TR (IN REF. 4).

CONFLICT 2 3 GS -> TR (IN REF. 4).

CONFLICT 2 3 GS -> TRSREPGRQEGCTR (IN REF. 2).

CONFLICT 84 84 G -> S (IN REF. 2, 3, 4 AND 5).

CONFLICT 231 232 YH -> SP (IN REF. 2).

CONFLICT 293 293 T -> P (IN REF. 2).

SEQUENCE 307 AA; 32168 MW; 567D32AE35BA44F CRC64;

Query Match 10.8%; Score 221; DB 1; Length 307;

Best Local Similarity 26.7%; Pred. No. 1.2e-10; Mismatches 119; Indels 46; Gaps 10;

Matches 76; Conservative 44; Mismatches 119; Indels 46; Gaps 10;

QY 7 RTLLALVCTFTYLLVGAAPDALESEP--ELIERORLELRQOEIRARVNLSSGGYEELER 64

Db 9 RYLLLLAAHLLAMGLGAVVLALEGPARRHLQAVQAEHLASFOAEHRACLPPEALEELLG 68

QY 65 VVLRKPKHAGV-----QMRFAGSYFAITVTTTGYGHADPSTDGKVFCEMFA 114

Db 69 AVLRQAQH--GVSSLSGSETSNWDLPSALLFTASILTITTYGGMADPLSSGKAFQVYA 126

QY 115 ILGPIPLVMEOSL-----GRINTIVRYLLHRAKKGLGMRADYSMANMVLIG 163

Db 127 ALGIPASLAAVAALRHCLLPVSRPGDV--AIRWQAPAOAL-----LQAGLGLL- 177

QY 164 FFSCTISTCIGAAAFSHEHMTFFQAVYCYFTLTITGFDYVALQ--KDOALOTOPQY 220

Db 178 -VACVFLRLALVLMGQVQSCSLLEATYFCGSLSTIGLDLPAHGRGLHAPATYHLOF 236

QY 221 VAESEVY--ILTGLTVIGAFNLVLRFTM-----NADEKRD 257

Db 237 ALGTYLLGLLAMLAVETSELPQVRAMVKFGPSSGRTDEDD 281

Search completed: August 28, 2001, 17:13:15  
 Job time: 409 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 28, 2001, 17:12:46 ; Search time 54.36 Seconds

(without alignments)  
958.944 Million cell updates/sec

Title: US-09-503-089A-5

Perfect score: 2042  
Sequence: 1 MKRQNVRLTALIVCTFTYLL.....STGLHSLSTFRGLMKRRSSV 394

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: SPREMBL\_16:\*  
2: SP\_archaea:\*  
3: SP\_bacteria:\*  
4: SP\_fungi:\*  
5: SP\_human:\*  
6: SP\_invertebrate:\*  
7: SP\_mammal:\*  
8: SP\_mhc:\*  
9: SP\_organelle:\*  
10: SP\_phage:\*  
11: SP\_plant:\*  
12: SP\_protent:\*  
13: SP\_unclassified:\*  
14: SP\_vertebrate:\*  
15: SP\_virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1732	84.8	392	11	Q9ESM5
2	1333	65.3	299	11	Q9QX34
3	1298.5	63.6	301	11	Q9ESM4
4	1116	54.7	374	4	Q9NPC2
5	1069.5	52.4	365	11	Q9JL58
6	960.5	47.0	395	11	Q9JL58
7	924	45.2	337	11	Q9JL58
8	846	41.4	330	4	Q9HBC8
9	838	41.0	330	4	Q9H427
10	820	40.2	329	5	Q9H427
11	806.5	39.5	336	5	Q9H427
12	777	38.1	340	5	Q9H427
13	742	36.3	398	5	Q9H427
14	732.5	35.9	270	11	Q9JL57
15	599	29.3	364	5	Q9JL57
16	369	18.1	405	11	Q9ERS0
17	363	17.8	411	4	Q9H591
18	361	17.7	294	4	Q9H591
19	357.5	17.5	408	4	Q9H514

20	349.5	17.1	538	4	Q9H591
21	349.5	17.1	538	11	Q9JL54
22	324	15.9	502	11	Q9JL54
23	319.5	15.6	336	11	Q9JL54
24	310.5	15.2	430	4	Q9H515
25	309.5	15.2	430	11	Q9ERS1
26	307.5	15.1	513	5	Q9ERS1
27	302	14.8	259	5	Q9ERS1
28	293	14.3	293	4	Q9H592
29	288	14.1	229	4	Q9H592
30	281.5	13.8	385	5	Q9H592
31	278.5	13.6	592	5	Q9H592
32	278.5	13.6	995	5	Q9H592
33	276.5	13.5	313	11	Q9ERS5
34	276.5	13.5	1910	5	Q9ERS5
35	275	13.5	524	5	Q9ERS5
36	268	13.1	1539	5	Q9ERS5
37	262	12.8	443	5	Q9ERS5
38	258.5	12.7	427	5	Q9ERS5
39	258	12.6	383	5	Q9ERS5
40	256.5	12.6	452	5	Q9ERS5
41	251.5	12.3	389	5	Q9ERS5
42	251	12.3	498	5	Q9ERS5
43	251	12.3	512	5	Q9ERS5
44	251	12.3	544	5	Q9ERS5
45	251	12.3	562	5	Q9ERS5

## ALIGNMENTS

RESULT	ID	Query Match	Similarity	Score	Length	DB	Indels	Gaps
1	Q9ESM5	84.8%	83.9%	1732	392	11	36	4
2	Q9ESM5	65.3%	63.6%	1298.5	301	11	36	4
3	Q9ESM5	63.6%	63.6%	1298.5	301	11	36	4
4	Q9NPC2	54.7%	54.7%	1116	374	4	36	4
5	Q9JL58	52.4%	52.4%	1069.5	365	11	36	4
6	Q9JL58	47.0%	47.0%	960.5	395	11	36	4
7	Q9JL58	45.2%	45.2%	924	337	11	36	4
8	Q9HBC8	41.4%	41.4%	846	330	4	36	4
9	Q9H427	41.0%	41.0%	838	330	4	36	4
10	Q9H427	40.2%	40.2%	820	329	5	36	4
11	Q9H427	39.5%	39.5%	806.5	336	5	36	4
12	Q9H427	38.1%	38.1%	777	340	5	36	4
13	Q9H427	36.3%	36.3%	742	398	5	36	4
14	Q9JL57	35.9%	35.9%	732.5	270	11	36	4
15	Q9JL57	29.3%	29.3%	599	364	5	36	4
16	Q9ERS0	18.1%	18.1%	369	405	11	36	4
17	Q9H591	17.8%	17.8%	363	411	4	36	4
18	Q9H591	17.7%	17.7%	361	294	4	36	4
19	Q9H514	17.5%	17.5%	357.5	408	4	36	4

QY	241	LVLFEMTNNADEKDAHRAHLLTNGOAGGGG	-----GGAHNTTDAASAAA	291
DB	222	LVLFEMTNNADEKDAHRAHLLTNGOAGGIGGISCISGSLGSDVRRPDPYTCAAAG	281	
QY	292	-----GGGFFRVNVAEVLHFQSMCSGLMKSRREKLOYSDIPMIIPRLSTSDTCVEOS	343	
DB	282	GMGVGVGVGSGSFFRVNVAEMLHFQSMCSGLMKSRREKLOYSDIPMIIPRLSTSDTCVEOS	341	
QY	344	HSSPGGGGSDPTPSRRCISGAPRSATISVSTGLHSTFPGIMRRSSV	394	
DB	342	HSSPGGGGSDPTPSRRCISGAPRSATISVSTGLHSTFPGIMRRSSV	392	
RESULT	2			
Q90X34	ID	Q90X34	PRELIMINARY:	PRT: 299 AA.
AC	Q90X34:			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)			
DE	PURATIVE POTASSIUM CHANNEL DP4 (FRAGMENT).			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RA	Gan L., Joiner W.J., Quin A.M., Wang L.-Y., Hughes T.,			
RA	Kacmarek L.K.;			
RL	Submitted (SEP-1997) to the EMBL/Genbank/DBJ databases.			
DR	EMBL, AF022821; AAD09338.1; --			
DR	InterPro; IPR000099; --			
DR	InterPro; IPR001622; --			
DR	InterPro; IPR003092; --			
DR	InterPro; IPR003280; --			
DR	Pfam; PF02034; TWIK_channel.1.			
DR	PRINTS; PRO1333; 2PORECHANNEL.			
DR	PRINTS; PRO1095; TASKCHANNEL.			
KW	ionic channel.			
FT	NON_TER	1		
FT	NON_TER	299		
SEQUENCE	299 AA; 33325 MW; DCD41D8A212939C4 CRC64;			
Query Match	65.3%;	Score 1333;	DB 11;	Length 299;
Best Local Similarity	88.9%;	Pred. No. 7.8e-110;		
Matches 263; Conservative	7;	Mismatches 18;	Indels 8;	Gaps 1
QY	4	ONVRLTALVCFEFTLLVCAAVFDALLESPELIERQLRLROELRARNLISOGGYEELE	63	
DB	2	ENVRLLALVCFEFTLLVGAAVFDALLESPEMIERQLRLROELRARNLISOGGYEELE	61	
QY	64	RVVLRLLPKHAKGVQWRFAVSFFFAITVITITIGVHAAPSTDGKVCMPYALGIPLTLY	123	
DB	62	RVVLRLLPKHAKGVQWRFAVSFFFAITVITITIGVHAAPSTDGKVCMPYALGIPLTLY	121	
QY	124	MFQSGIGERINTLVYLLHRAKGLGRRADVSMANNVLTIGFSCISTLCIGAASHYEH	183	
DB	122	MFQSGIGERINTLVYLLHRAKGLGRRADVSMANNVLTIGFSCISTLCIGAASHYER	181	
QY	184	WFFPDAYVYCFEFTLLTIGGVDVVALOKDQALOTOPQYVAFSVYVILITGLTVGAFINTLV	243	
DB	182	WFFPDAYVYCFEFTLLTIGGVDVVALOKDQALOTOPQYVAFSVYVILITGLTVGAFINTLV	241	
QY	244	LRFMTMAEDEKRAEHRALLTRNGOAGGGG-----GGAHNTTDAASAAA	291	
DB	242	LRFMTMAEDEKRAEHRALLTRNGOAGVGLSCLSGSLGSDVRRPDPYTCAAAA	297	
RESULT	3			
Q9ESM4	ID	Q9ESM4	PRELIMINARY:	PRT: 301 AA.

AC	Q9ESM4	01-MAR-2001 (TREMblrel. 16, Created)
DT	01-MAR-2001 (TREMblrel. 16, last sequence update)	
DT	01-MAR-2001 (TREMblrel. 16, last sequence update)	
DT	01-MAR-2001 (TREMblrel. 16, last sequence update)	
DE	TWIK-RELATED ACID-SENSITIVE K+ CHANNEL SPLICING VARIANT (TASK1C).	
GN	KCNK3C.	
OS	Rattus norvegicus (Rat).	
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	
OX	NCBI_TaxID=10116;	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=ADRA;	
RA	Ohya S., Kutsukawa M., Imaizumi Y.;	
RT	"TWIK-related acid-sensitive K+ channel (TWIK) (KCNK3) splice variant."	
RL	Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.	
DR	EMBL; AB048824; BAB16711.1;	
KW	Ionic channel.	
SO	SEQUENCE 301 AA; 32811 MW; 265DE38DFA79595F CRC64;	
QY	111 MEVALGIPPLTVMQSGERINTLVRYLLHAKKGLGDKHRRVDSMANNVLLGFSCIST 170	
Db	1 MEVALGIPPLTVMQSGERINTLVRYLLHAKKGLGDKHRRVDSMANNVLLGFSCIST 60	
QY	171 LCIGAAAFSHYEHMTFPOAYYYCFTLTITIGFGDYVALQNT ALOTPODYAFSEVYILT 230	
Db	61 LCIGAAAFSHYEHMTFPOAYYYCFTLTITIGFGDYVALQNT ALOTPODYAFSEVYILT 120	
QY	231 GLTYVGAFLNLVLRFTMTNAEDERDAEHRALLTRNGCAGCGG-----GGSANTT 282	
Db	121 GLTYVGAFLNLVLRFTMTNAEDERDAEHRALLTRNGCAGCGG-----GGSANTT 180	
QY	283 DTASSTAA-----GGGGRNVVAEVLHFOGMSCLMVKSRKLOYSTPMIIPRL 333	
Db	181 DPVTCMAAAGMGVGVGGSGFRNVVEMHLPFGMSCLMVKSRKLOYSTPMIIPRL 240	
QY	334 STSDPCVEQSHSSPGGGGRVSDTPESRRLCGAPSAISLV GHLSLTFEGLKKRRSS 393	
Db	241 STSDPCVEHSHSSPGGGGRVSDTPESRRLCGSTQKSAISLSVIGHLSLATIFGLKKRRSS 300	
QY	394 V 394	
Db	301 V 301	
RESULT	4	
Q9NPC2	PRELIMINARY; PRT; 374 AA.	
AC	Q9NPC2;	
DT	01-OCT-2000 (TREMblrel. 15, Created)	
DT	01-OCT-2000 (TREMblrel. 15, last sequence update)	
DT	01-MAR-2001 (TREMblrel. 16, last annotation update)	
DE	2P DOMAIN POTASSIUM CHANNEL TASK-3 (POTASSIUM CHANNEL TASK3) (TWO PORE	
GN	POTASSIUM CHANNEL KT3.2) (2P DOMAIN POTASSIUM CHANNEL).	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.	
OX	NCBI_TaxID=9606;	
RP	SEQUENCE FROM N.A.	
RA	Girard C., Lesage F., Tinel N., Lazdunski M.;	
RT	"Human Task-3, a novel 2P domain potassium channel related to Task.3";	
RL	Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.	
RN	SEQUENCE FROM N.A.	
RX	MEDLINE=20287530; PubMed=10747866;	

```

evy Match          63.6%   Score 1298..5;   DB 11;   Length 301;
    Local Similarity 85.0%;   Pred No. 8..8e-17;
atches 256;   Conservative 6;   Mismatches 22;   Indels 17;   Gaps
      2.

111 MEYALIGDPLVLMFOSLGERINTLVRYLLHRAKKGAGKRAIVSMANNVLIGFSCIST 170
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1 MEYALIGILTLVMEFOSLSGERINTEVRYLHLHAKRKGRHH;EVSMAENVLLIGFVCISIT 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

171 LCIGAANAFHYEHMFPEOAYYYCCFTLTITIGRDYVALCNC;ALQOPOPYAFSPFYILT 230
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
61 LCIGAANAFHYERMTFFQAYYYCFITLTITIGGDYVALCKDJALOTOPPYAFSPFYIILT 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

231 GLTVIGAFNLVLYLRMTNNAEDKRDAEHRALLTRNGCAAGCGG-----GGSAHTT 282
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
121 GLTVIGAFNLVLYLRMTNNAEDKRDAEHRALLTHNGCAAGGLSGLSGSIGSGVRPR 180
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

283 PRASSTAAA-----GGGFRRNYAEVLAHFQSMCSCLMKRSREKLQYSTPIIPRLD 333
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
181 DPVTCAAAGGAGGVGVSGFRNVYAEMLFHQSMCSCLNK;KSREKLQYSTPIIPRLD 240
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

334 STSDPCVEBSSHSPGGGGGRTDPSPSRRCSCSAPRGAISYS;GLHSISTFGFLKKRRSS 393
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
241 STSDPCVEBSSHSPGGGGGRTDPSPSRRCSCSGLTORSAISSVSLGLHSIATFGFLKKRRSS 300
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

394 V 394
|
301 V 301

LT 4
C22
09NPC2 PRELIMINARY; PRT; 374 AA.
09NPC2:
01-OCT--2000 (TREMBLrel. 15, Created)
01-OCT--2000 (TREMBLrel. 15, Last sequence update)
01-MAR-2001 (TREMBLrel. 16, Last annotation update)
2P DOMAIN POTASSIUM CHANNEL TASK-3 (POTASSIUM CHANNEL TASK3) (TWO PORE
POTASSIUM CHANNEL KTJ3.2) (2P DOMAIN POTASSIUM CHANNEL).
KCNE9.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxId=9606;
[1]
SEQUENCE FROM N.A.
Girard C., Lesage F., Tinel N., Lazdunski M.;
"Human Task-3, a novel 2P domain potassium channel related to Task.";
Submitted (Jun-2000) to the EMBL/GenBank/DDBJ databases.
[2]
SEQUENCE FROM N.A.
MEDLINE=20287530; PubMed=10747866;
```

RA Rajan S., Wischmeyer E., Liu G.X., Preisig-Mueller R., Daut J.,  
 RA Karschin A., Derst C.;  
 RT "TASK-3, a novel tandem proe domain acid-sensitive K<sup>+</sup> channel. An  
 RT extracellular histidine as pH sensor.";  
 RT J. Biol. Chem. 275:16650-16657(2000).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Vega-Saenz de Miera E.C., Lau D.H.P., Zhadina M., Pountney D.,  
 RA Coetzee W., Rudy B.;  
 RT "K7.2 and K7.3 Two Novel Human Two Pore K<sup>+</sup> Channels Closely Related  
 RT to TASK1.";  
 RT Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-BRAIN;  
 RX PubMed-11042359;  
 RA Chapman C.G., Meadows H.J., Godden R.J., Campbell D.A., Duckworth M.,  
 RA Kelsell R.E., Mordock P.R., Randall A.D., Rennie G.I., Gloger I.S.;  
 RT "Cloning, localisation and functional expression of a novel human,  
 RT cerebellum specific, two pore domain potassium channel.";  
 RL Brain Res. Mol. Brain Res. 82:74-83(2000).  
 DR EMBL: AF279809; AAF85982.1; -;  
 DR EMBL: AF257080; AAG33126.1; -;  
 DR EMBL: AF248241; AAG31730.1; -;  
 DR InterPro: IPR000099; -;  
 DR InterPro: IPR001622; -;  
 DR InterPro: IPR003092; -;  
 DR InterPro: IPR003280; -;  
 DR Pfam: PF02034; TWIK\_channel; 1.  
 DR PRINTS: PRO1333; ZPORECHANNEL.  
 DR PRINTS: PRO1095; TASKCHANNEL.  
 KW Ionic channel.  
 SQ SEQUENCE 374 AA; 42263 MW; 8A19EAEE5AD7F38 CRC64;

Query Match 54.78; Score 1116; DB 4; Length 374;  
 Best Local Similarity 59.08; Pred. No. 1.5e-90;  
 Matches 233; Conservative 44; Mismatches 96; Indels 22; Gaps 5;

QY 1 MKRONVRLIALVCTFTYLLVGAAVFDALSEPELIERORLELROQELRARVYNSOGYE 60  
 DB 1 MKRONVRLIALVCTFTYLLVGAAVFDALSEPELIERORLELROQELRARVYNSOGYE 60  
 QY 61 ELERVLRLKPKHAKGVOMRFAGSFYFAITVTTTIGYHAAPSTDGKVFCAAFYALGIP 120  
 DB 61 ELERVLRLKPKHAKGVOMRFAGSFYFAITVTTTIGYHAAPSTDGKVFCAAFYALGIP 120  
 QY 61 QLELVIIQSEPHRAGVOMKFGSFYFAITVTTTIGYHAAPSTDGKVFCAAFYALGIP 120  
 DB 61 QLELVIIQSEPHRAGVOMKFGSFYFAITVTTTIGYHAAPSTDGKVFCAAFYALGIP 120  
 QY 121 TLVNFQSLGERINLVRLHRAKGLGMRRADVSMANVLI GFSCISTLCIGAAAFSH 180  
 DB 121 TLVNFQSLGERINLVRLHRAKGLGMRRADVSMANVLI GFSCISTLCIGAAAFSH 180  
 QY 121 TLVNFQSLGERINLVRLHRAKGLGMRRADVSMANVLI GFSCISTLCIGAAAFSH 180  
 DB 121 TLVNFQSLGERINLVRLHRAKGLGMRRADVSMANVLI GFSCISTLCIGAAAFSH 180  
 QY 181 YEHTFFQAYYCFITLTITGFGDYVALQKQALOTQPOYAFSEVYILTLGTYIGAF 240  
 DB 181 YEHTFFQAYYCFITLTITGFGDYVALQKQALOTQPOYAFSEVYILTLGTYIGAF 240  
 QY 181 YEHTFFQAYYCFITLTITGFGDYVALQKQALOTQPOYAFSEVYILTLGTYIGAF 240  
 DB 181 YEHTFFQAYYCFITLTITGFGDYVALQKQALOTQPOYAFSEVYILTLGTYIGAF 240  
 QY 241 LVVLRFTMNAEDKRDRAEHRALLTRNGOAGGGGSAHTTDPASSTAAAGGGGFRNV 300  
 DB 241 LVVLRFTMNAEDKRDRAEHRALLTRNGOAGGGGSAHTTDPASSTAAAGGGGFRNV 300  
 QY 241 LVVLRFTMNAEDKRDRAEHRALLTRNGOAGGGGSAHTTDPASSTAAAGGGGFRNV 300  
 DB 241 LVVLRFTMNAEDKRDRAEHRALLTRNGOAGGGGSAHTTDPASSTAAAGGGGFRNV 300  
 QY 301 -AEVLHROSQSCSLMYKSRKLOYSIPMIIPROLDSTDCVEGSHSPGGGGRYSDPSP 359  
 DB 301 -AEVLHROSQSCSLMYKSRKLOYSIPMIIPROLDSTDCVEGSHSPGGGGRYSDPSP 359  
 QY 301 -AEVLHROSQSCSLMYKSRKLOYSIPMIIPROLDSTDCVEGSHSPGGGGRYSDPSP 359  
 DB 301 -AEVLHROSQSCSLMYKSRKLOYSIPMIIPROLDSTDCVEGSHSPGGGGRYSDPSP 359  
 QY 360 RCLCSGAPRAISSVSTGLSLSTFRGLMKRRSSV 394  
 DB 360 RCLCSGAPRAISSVSTGLSLSTFRGLMKRRSSV 394  
 QY 360 RCLCSGAPRAISSVSTGLSLSTFRGLMKRRSSV 394  
 DB 360 RCLCSGAPRAISSVSTGLSLSTFRGLMKRRSSV 394  
 QY 344 NSLFP-----SPITSSIPGLSHFTDQRLMKRRKSV 374  
 DB 344 NSLFP-----SPITSSIPGLSHFTDQRLMKRRKSV 374

RESULT 5  
 ID 09JL58 PRELIMINARY; PRT; 365 AA.  
 AC 09JL58;  
 OC 09JL58;

DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation)  
 DE POTASSIUM CHANNEL TASK3.  
 CN KCN9.  
 OS Cavia porcellus (Guinea pig).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Hystricognath; Caviidae; Cavia.  
 NX NCBI\_TaxID=10141;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-BRAIN;  
 RX MEDLINE=20287530; PubMed-10747866;  
 RA Rajan S., Wischmeyer E., Liu G.X., Preisig-Mueller R., Daut J.,  
 RA Karschin A., Derst C.;  
 RT "TASK-3, a novel tandem proe domain acid-sensitive K<sup>+</sup> channel. An  
 RT extracellular histidine as pH sensor.";  
 RL J. Biol. Chem. 275:16650-16657(2000).  
 DR EMBL: AF212827; AAF63706.1; -;  
 DR InterPro: IPR000099; -;  
 DR InterPro: IPR001622; -;  
 DR InterPro: IPR003092; -;  
 DR InterPro: IPR003280; -;  
 DR Pfam: PF02034; TWIK\_channel; 1.  
 DR PRINTS: PRO1333; ZPORECHANNEL.  
 DR PRINTS: PRO1095; TASKCHANNEL.  
 SQ SEQUENCE 365 AA; 40769 MW; 261DC973FF5 CRC64;

Query Match 52.48; Score 1069.5; DB 4; Length 365;  
 Best Local Similarity 57.18; Pred. No. 1.9e-90;  
 Matches 226; Conservative 43; Mismatches 96; Indels 33; Gaps 6;

QY 1 MKRONVRLIALVCTFTYLLVGAAVFDALSEPELIERORLELROQELRARVYNSOGYE 60  
 DB 1 MKRONVRLIALVCTFTYLLVGAAVFDALSEPELIERORLELROQELRARVYNSOGYE 60  
 QY 61 ELERVLRLKPKHAKGVOMRFAGSFYFAITVTTTIGYHAAPSTDGKVFCAAFYALGIP 120  
 DB 61 ELERVLRLKPKHAKGVOMRFAGSFYFAITVTTTIGYHAAPSTDGKVFCAAFYALGIP 120  
 QY 61 QLELVIIQSEPHRAGVOMKFGSFYFAITVTTTIGYHAAPSTDGKVFCAAFYALGIP 120  
 DB 61 QLELVIIQSEPHRAGVOMKFGSFYFAITVTTTIGYHAAPSTDGKVFCAAFYALGIP 120  
 QY 121 TLVNFQSLGERINLVRLHRAKGLGMRRADVSMANVLI GFSCISTLCIGAAAFSH 180  
 DB 121 TLVNFQSLGERINLVRLHRAKGLGMRRADVSMANVLI GFSCISTLCIGAAAFSH 180  
 QY 121 TLVNFQSLGERINLVRLHRAKGLGMRRADVSMANVLI GFSCISTLCIGAAAFSH 180  
 DB 121 TLVNFQSLGERINLVRLHRAKGLGMRRADVSMANVLI GFSCISTLCIGAAAFSH 180  
 QY 181 YEHTFFQAYYCFITLTITGFGDYVALQKQALOTQPOYAFSEVYILTLGTYIGAF 240  
 DB 181 YEHTFFQAYYCFITLTITGFGDYVALQKQALOTQPOYAFSEVYILTLGTYIGAF 240  
 QY 181 YEHTFFQAYYCFITLTITGFGDYVALQKQALOTQPOYAFSEVYILTLGTYIGAF 240  
 DB 181 YEHTFFQAYYCFITLTITGFGDYVALQKQALOTQPOYAFSEVYILTLGTYIGAF 240  
 QY 241 LVVLRFTMNAEDKRDRAEHRALLTRNGOAGGGGSAHTTDPASSTAAAGGGGFRNV 298  
 DB 241 LVVLRFTMNAEDKRDRAEHRALLTRNGOAGGGGSAHTTDPASSTAAAGGGGFRNV 298  
 QY 241 LVVLRFTMNAEDKRDRAEHRALLTRNGOAGGGGSAHTTDPASSTAAAGGGGFRNV 298  
 DB 241 LVVLRFTMNAEDKRDRAEHRALLTRNGOAGGGGSAHTTDPASSTAAAGGGGFRNV 298  
 QY 299 VYAEVLHROSQSCSLMYKSRKLOYSIPMIIPROLDSTDCVEGSHSPGGGGRYSDPSP 358  
 DB 299 VYAEVLHROSQSCSLMYKSRKLOYSIPMIIPROLDSTDCVEGSHSPGGGGRYSDPSP 358  
 QY 299 VYAEVLHROSQSCSLMYKSRKLOYSIPMIIPROLDSTDCVEGSHSPGGGGRYSDPSP 358  
 DB 299 VYAEVLHROSQSCSLMYKSRKLOYSIPMIIPROLDSTDCVEGSHSPGGGGRYSDPSP 358  
 QY 359 RCLCSGAPRAISSVSTGLSLSTFRGLMKRRSSV 394  
 DB 359 RCLCSGAPRAISSVSTGLSLSTFRGLMKRRSSV 394  
 QY 359 RCLCSGAPRAISSVSTGLSLSTFRGLMKRRSSV 394  
 DB 359 RCLCSGAPRAISSVSTGLSLSTFRGLMKRRSSV 394  
 QY 332 --TLKNSLFPSPISVSFGLSHFDQRLMKRRKSV 365  
 DB 332 --TLKNSLFPSPISVSFGLSHFDQRLMKRRKSV 365

RESULT 6  
 ID 09JL58 PRELIMINARY; PRT; 395 AA.  
 AC 09JL58;  
 OC 09JL58;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation)  
 DE POTASSIUM CHANNEL TASK3.  
 CN KCN9.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.



DT 01-MAR-2001 (TREMblrel\_16, last annotation update)  
DE DJ781B1.1 (A NOVEL PROTEIN SIMILAR TO THE ACID-SENSITIVE POTASSIUM  
DE CHANNEL PROTEIN TASK (KCNK3)).  
GN DJ781B1.1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP  
RA Lovell J.;  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AL118532; CAC14068.1; -  
SO SEQUENCE 330 AA; 3622 MW; 24F428721A1C7790 CRC64; .

Query Match	41.0%;	Score 838;	DB 4;	Length 330;
Best Local Similarity	-64.3%;	Pred. NO. 4.8e-66;		
Matches 166;	Conservative 32;	Mismatches 60;	Indels 0;	Gaps 0;

[illegible]

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RESULT      10
ID           076795
AC           076795;
DT           01-NOV-1998 (TEMBLrel. 08, Created)
DT           01-NOV-1998 (TEMBLrel. 08, last sequence update)
DT           01-MAR-2001 (TEMBLrel. 16, last annotation update)
DE           PUTATIVE POTASSIUM CHANNEL SUBUNIT N2P38.
OS           Caenorhabditis elegans.
OC           Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae.
OC           Rhabditidae; Peloderinae; Caenorhabditis.
OX           NCBI_TaxID=6239;
RN           [1]
RP           SEQUENCE FROM N.A.
RA           Wang Z.-W., Salkoff L.;
RT           "Potassium channels in C. elegans.";
RL           Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR           EMBL; AF083652; AAC32863.1; -.
DR           InterPro; IPR000099; -.
DR           InterPro; IPR001622; -.
DR           InterPro; IPR003280; -.
DR           Pfam; PF02034; TWIK_channel.1.
DR           PRINTS; PR01333; 2PORECHANNEL.
KW           Ionic channel.
SQ           SEQUENCE      329 AA;  36992 MW;  338A6D9A577464CD CRC64;

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Query Match	40.2%;	Score 820;	DB 5;	Length 329;
Best Local Similarity	48.3%;	Pred. No. 1.8e-64;		
Matches 172;	Conservative 54;	Mismatches 84;	Indels 46;	Gaps 7;

Db 1 MKRQRIKLSLIVCTITLTLVGAFAVDALFENELIQRKLVQKREKLRIKYNMSNDYE 60

Qy 61 ELERVVLRLKPKHGVQWRFAGSEFYALITTTTIGYGHAPSVDGHWFCMFLVALLGIPL 120

Db 61 ILEAVIVSVPKHAGVQWKFSGAFYFATVITTTIGYGHSPFRDAGWFCMLVALLGIPL 120

Qy 121 TLVWQSGIKELINTLVRLILHRAKKGLGMRADVSMANVTFSCSLITLC--GAAAF 178

Db 121 GLIMQSIGEMRNFFAAKLIFERRAG-KPIYTSSIFCTGNGGLLFGGAFMF 177

Qy 179 SHYEHTFFQAYVYCFITLTIGFGDYVALOKDQALOTVAFSEVYLITGLTVGAF 238

Db 178 SSEKMTYFEDAVYVCFVLTITIGFGDYVALOKRSLQIVAFSLVLTLPGLTVISAA 237

Qy 239 LNLVVLRFMTNAADDEKRDAAHRLL---LTRNQACGSAHITDPAASSTAANGG 294

Db 238 MNLVLRLRLTNTDEDERDEDEALIAAGLVAVDPATAHRLPDSNVSTLAS----- 292

Qy 295 GFRNVYAEVLHFGQSCSLWAKSKREKLOYTSLPIIPIRIYICVEQSHSPQGG 350

Db 293 ---CSC-YQLPDEKLRH---HRKHTPEHGG 316

ID	RESULT	11
017185	PRELIMINARY;	PRT; 336 AA.
AC	017185.	
DT	01-JAN-1998 (TrEMBLrel. 05, Created)	
DT	01-JAN-1998 (TrEMBLrel. 05, Last sequence update)	
DT	01-MAR-2001 (TrEMBLrel. 16, Last annotation update)	
DE	F34D6.3 PROTEIN.	
GN	F34D6.3.	
OS	Caenorhabditis elegans.	
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;	
OC	Rhabditidae; Pelodermidae; Caenorhabditis.	
OX	NCBI_TaxID=6239;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RP	STRAIN-BRISTOL N2.	
RC	MEDLINE=94150718; PubMed=7906398;	
RX	Wilson R, Ainscough R, Anderson K, Bayne M, Berkis M, Bonfield J, Burton J, Connell M, Copsey J, Cooper J, Coulson A, Craxton M, Dear S, Du Z, Durbin R, Fawcett J, Fulton L, Gardner A, Green P, Hawkins T, Hillier L, Jones M, Kershaw J, Kirsten J, Laister N, Latham J, Liddle C, Marshall M, Martin J, McMurtry A, Mortimer J, O'Callaghan M, Parsons J, Percy C, Rifkin A, Roopra A, Smailton N, Smith A, Sonhammer E, Strader T, Thierry-Mieg J, Thomas K, Vaudin M, Vaux S, Watson A, Weinstock L, Wilkinson-Spratt J, Wollman P, "2.2 Mb of contiguous nucleotide sequence of chromosome III of C. elegans."	
RL	Nature 368:32-38(1994).	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RP	STRAIN-BRISTOL N2.	
RC	Murray J, Wohlmann P, O'Neal D.	
RL	Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.	
RN	[3]	
RP	SEQUENCE FROM N.A.	
RP	STRAIN-BRISTOL N2;	
RC	Waterston R.	
RL	Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.	
DR	EMBL; AF025454; AAC71151.1;	
DR	InterPro: IPR000099;	
DR	InterPro: IPR001622;	
DR	InterPro: IPR003280;	
DR	Pfam; PF02034; TWIK_channel; 1.	
DR	PRINTS; PR01333; 2P0RECHANNEL.	
DR	SEQUENCE 336 AA; 37700 MW; E0474024F69F727E CRC64;	





RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Manalidis P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA April J.F., Agbayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,  
RA Bailey R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Fjosek A., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
RA Jallali M., Kalush F., Kapran G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacile J.M.,  
RA Palazolo D.R., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Schaefer F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spletter E., Spredling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
RA Williams S.M., Woodage T., Morley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
RA "The genome sequence of *Drosophila melanogaster*."  
RT Science 287:2185-2195(2000).  
RL EMBL: AEO03701; AAF54970.1;  
DR FLYBase: FBgn0038165; CG9637.  
DR InterPro: IPR000099;  
DR InterPro: IPR001622;  
DR InterPro: IPR003092;  
DR Pfam: PF02034; TWIK channel; 1.  
DR PRINTS: PRO1095; TASKCHANNEL.  
SQ SEQUENCE 398 AA; 44269 MW; D5DC01E9DBA6D7E CRC64;

Query Match 36.3%; Score 742; DB 5; Length 398;  
Best Local Similarity 42.8%; Pred. No. 1.8e-57;  
Matches 161; Conservative 65; Mismatches 76; Indels 74; Gaps 9;  
QY 1 MKRONVRLIIVCTFTYLLVGAIVFDALSEPELIERORLEKQOEIRARNISOGYE 60  
DB 1 MKKONVRLISIVCTFTYLLVGAIVFDALSEPELIERORLEKQOEIRARNISOGYE 60  
QY 61 ELERVLRLKHKAGVDFGAFYFATVTTTGCGHAFSDGKCFKCFVALLGPL 120  
DB 61 VMEIVVLKSEHKAGQCKFGAFYATVTTTGCGHAFSDGKCFKCFVALLGPL 120  
QY 121 TLVNFOSLGERINTLVRYLRLHARKGLGMRADYSMANVLIIGFSCISTLCI--GAANF 178  
DB 121 GLVNFOSLGERINTLVRYLRLHARKGLGMRADYSMANVLIIGFSCISTLCI--GAANF 178  
QY 179 SHYEWTFFOAYYYCFTLTITIGFDYVALOKDALOTPOYVAFSPYITLGLVIGAF 238  
DB 179 SKFGWSTFYDSVYCFITLTITIGFDYVALQDNLNRPYVAFSPYITLGLVIGAF 238  
QY 239 LNLVLRPMTNNADEKDAEHRAL-----LTERNGAGGGGGGSAHTTDTA 285  
DB 239 LNLVLRPMTNNADEKDAEHRAL-----LTERNGAGGGGGGSAHTTDTA 285  
QY 286 SSTAAAGGGGRNVYAEVLAHFQSMCSC-----LWYSREK-- 320

DB 288 NTS-----SMCSCHICLGNRHH-----EKNDAENQYLRSPPT 328  
QY 321 -LOYSIPIIP-RDLS 334  
DB 329 HIRLLEPVPMDLN 344  
RESULT 14  
ID 09JUL57 PRELIMINARY; PRT: 270 A  
AC 09JUL57  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence  
DT 01-MAR-2001 (TREMBlrel. 16, last annotatio  
DE POTASSIUM CHANNEL TASK3 (FRAGMENT).  
GN KCNK9.  
OS Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Ve  
OC Mammalia; Eutheria; Rodentia; Hystriognath  
OX NCBI\_TaxID=10141;  
RN 11  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20287530; PubMed=10747866;  
RA Rajan S., Wilschmeyer E., Liu G.X., Preisig  
RA Rajan S., Wilschmeyer E., Liu G.X., Preisig  
RT "TASK-3, a novel tandem proe domain acid-  
RT extracellular histidine as pH sensor."  
J Biol. Chem. 275:16650-16657(2000).  
DR EMBL: AF212828; AAF63707.1;  
DR InterPro: IPR000099;  
DR InterPro: IPR001622;  
DR InterPro: IPR003092;  
DR Pfam: PF02034; TWIK channel; 1.  
DR PRINTS: PRO1095; TASKCHANNEL.  
FT NON\_TER 1 1  
SQ SEQUENCE 270 AA; 29658 MW; 092ABPFC67E CRC64;

Query Match 35.9%; Score 732.5;  
Best Local Similarity 54.2%; Pred. No. 7.8;  
Matches 163; Conservative 26; Mismatches 13; Indels 33; Gaps 6;  
QY 96 YGHAPSTDGKVCMEFALLGIPTLVFOSLGERIN-----LHRAKGLGMRADYS 155  
DB 1 YGHAPSTDGKVCMEFALLGIPTLVFOSLGERIN-----LHRAKGLGMRADYS 155  
QY 156 MANNVLIIGFSCISTLCIGAAGFHYEHWTFFOAYY-----FTGFDYVALOKDALQ 215  
DB 61 MENNVTVGFSCMGITLCIGAAGFHYEHWTFFOAYY-----FTGFDYVALOKDALQ 215  
QY 216 TOPQVAFSPYITLGLVIGAFPLNLVLRPMTNNAF-----EHRALLTNGAGGGGG 275  
DB 121 RKPEYVAFSPYITLGLVIGAFPLNLVLRPMTNNAF-----EHRALLTNGAGGGGG 275  
QY 276 GGSATHTDTASTAA--AGGGGRNVYAEVLAHFQSMC-----KSNKLOYSIPILIPDL 333  
DB 175 SVVTHISEAAGVQNRHYGEGG-----DLQSVG-----YRSP--QNGCATLAPPL 223  
QY 334 STSDTCVQSHSSPQGGGGGYSDDPSRRLCSGAPRSA-----VSGLHSITRGKLMKRRSS 393  
DB 224 HSIQRIEEL-----SPS--TLKNSLPSP-----SPSHSGFDNHRMLLRKRS 269  
QY 394 V 394  
DB 270 V 270  
RESULT 15  
ID 076790 PRELIMINARY; PRT: 364 A  
AC 076790;  
DT 01-NOV-1998 (TREMBlrel. 08, Created)

DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
 DE PUTATIVE POTASSIUM CHANNEL SUBUNIT N2P20.  
 GN TWK-4.  
 OS *Caenorhabditis elegans*.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
 OC Rhabditidae; Pelodierinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Wang Z.-W., Salcoff L.;  
 RT "Potassium channels in *C. elegans*."  
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Henry C.;  
 RT Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=99069613; PubMed=9851916;  
 RX none;  
 RA "Genome sequence of the nematode *C. elegans*: A platform for  
 RT investigating biology";  
 RL Science 282:2012-2018(1998).  
 DR EMBL, AF083646; AAC32857.1; -.  
 DR EMBL, Z70266; CAB61045.1; -.  
 DR InterPro: IPR000099; -.  
 DR InterPro: IPR001622; -.  
 DR InterPro: IPR003280; -.  
 DR Pfam: PF02034; TWIK\_channel; 1.  
 DR PRINTS: PR01333; 2PORECHANNEL.  
 KW Ionic channel.  
 SQ SEQUENCE 364 AA: 41374 MW: 424746050CCC4313 CRC64;

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 28, 2001, 17:06:26 ; Search time 21.03 Seconds  
(without alignments)  
669.472 Million cell updates/sec

Title: US-09-503-089a-2

Perfect score: 2100  
Sequence: 1 MAAPDLDPKSAONSKPRL.....LNGLTPHCAGEIAYENIK 411

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2062	98.2	426	CIW2_HUMAN	095069 homo sapien
2	2041	97.2	411	CIW2_MOUSE	P97438 mus musculu
3	803	38.2	393	CIW4_HUMAN	Q9ny98 homo sapien
4	776.5	37.0	398	CIW4_MOUSE	088454 mus musculu
5	427	20.3	499	CIW5_HUMAN	095279 homo sapien
6	379.5	18.1	336	CIW1_HUMAN	000180 homo sapien
7	370.5	17.6	336	CIW1_MOUSE	008581 mus musculu
8	363	17.3	394	CIW3_HUMAN	014649 homo sapien
9	348	16.6	313	CIW6_HUMAN	09y257 homo sapien
10	343	16.3	409	CIW3_MOUSE	035111 mus musculu
11	343	16.3	411	CIW3_RAT	054912 rattus norv
12	319	15.2	1001	ORX1_DROME	094556 drosophila
13	296.5	14.1	307	CIW8_MOUSE	092251 mus musculu
14	291.5	13.9	307	CIW7_HUMAN	Q9y242 homo sapien
15	217.5	10.4	335	TKW8_CAEEL	P34410 caenorhabdi
16	217.5	10.4	691	TKW1_YEAST	P40310 saccharomyc
17	121	5.8	228	YWS1_CAEEL	Q10937 caenorhabdi
18	120	5.7	676	CIW1_HUMAN	P51787 homo sapien
19	119	5.7	604	CIW1_MOUSE	P97414 mus musculu
20	106.5	5.1	334	PIT1_RHIME	030439 thizobium m
21	105.5	5.0	461	YIFK_SALTY	P37456 salmonella
22	104.5	5.0	649	QOX1_BACSU	P34956 bacillus su
23	102.5	4.9	362	SSRS_MOUSE	008858 mus musculu
24	102	4.9	402	Y718_METJA	058128 methanococ
25	102	4.9	451	Y5Y3_RHIME	033683 rhizobium m
26	101.5	4.8	342	COBD_SYNY3	P74475 synechocyst
27	100.5	4.8	352	Y436_METJA	Q57898 methanococ
28	100.5	4.8	476	MELB_SALTY	Q57898 salmonella
29	100	4.8	333	OAC_BPSF6	P23214 bacterioph
30	100	4.8	395	CDSA_MYCPN	P75160 m putative
31	100	4.8	567	COX1_EMENTI	P00402 emeticella
32	99.5	4.7	831	NAH3_RAT	P26433 rattus norv
33	99.5	4.7	834	NAH3_HUMAN	P48764 homo sapien

34	99.5	4.7	872	1	ATCL_MYCPN	P78036 mycoplasma
35	98.5	4.7	400	1	TYRP_HABIN	P44727 haemophilus
36	98.5	4.7	555	1	NRM1_CHICK	P51027 gallus gall
37	98.5	4.7	839	1	NAH3_DIDMA	028362 didelphis m
38	98	4.7	305	1	CDSA_MYCCE	049433 m putative
39	98	4.7	394	1	YDZC_SCHPO	010260 schizosacch
40	98	4.7	579	1	YH83_SCHPO	095522 schizosacch
41	97.5	4.6	412	1	085D_DROME	09vha2 drosophila
42	97.5	4.6	832	1	NAH3_RABIT	P26432 oryctolagus
43	97	4.6	333	1	Y13B_METJA	057604 methanococ
44	96.5	4.6	1036	1	SMD_DROME	P91682 drosophila
45	96	4.6	519	1	YF86_HABIN	P44263 haemophilus

## ALIGNMENTS

RESULT	1	STANDARD	PRT	426 AA
CIW2_HUMAN				
ID	095069	09UNE3		
AC	01-OCT-2000	(Rel. 40, Created)		
DF	01-OCT-2000	(Rel. 40, Last sequence update)		
DT	01-OCT-2000	(Rel. 40, Last annotation update)		
DE	POTASSIUM CHANNEL SUBFAMILY K MEMBER 2 (OUTW) RECTIFYING POTASSIUM CHANNEL TREK-1 (TWO-PORE POTASSIUM CHANNEL SUBUNIT).			
GN	KCNK2 OR TREK.			
OS	Homo sapiens (human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OX	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-99254548; PubMed-10321245;			
RA	Patel A.J., Honore E., Lesage F., Fink M., Hom G., Lazdunski M.;			
RT	"Inhalational anesthetics activate two-pore-domain background K <sup>+</sup> channels.";			
RL	Nat. Neurosci. 2:422-426(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TTSUDB-Brain;			
RA	Price L.A., Hellings S.E., Hayashi J.H., Patil M.H.;			
RL	Submitted (MAY-1997) to the EMBL/GenBank/DBI databases.			
CC	- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL.			
CC	- SUBUNIT: HOMODIMER (POTENTIAL).			
CC	- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE; CYTOSOL (POTENTIAL).			
CC	- MISCELLANEOUS: ACTIVATED BY VOLATILE GASES. ANAESTHETICS SUCH AS CHLOROFORM, HALOTHANE AND ISOFLURANE.			
CC	- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM CHANNELS.			
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CC	EMBL: AF129399; AAD47569.1; -			
DR	EMBL: AF004711; AAD01203.1; -			
DR	MM: 603219; -			
DR	InterPro: IPR000099; -			
DR	InterPro: IPR001622; -			
DR	InterPro: IPR003280; -			
DR	Pfam: PF02034; TWIK_Channel; 1.			
DR	PRINTS: PR01333; ZPORECHANNEL.			
KW	Ionic channel; Transmembrane; Ion transport; Potassium transport; Glycoprotein.			
KW	DOMAIN 1 61 CYTOPLASMIC (POTENTIAL).			
FT	TRANSMEM 62 82 POTENTIAL.			
FT	DOMAIN 144 170 PORE-FORMING (EXTRACELLULARITY).			

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FT TRANSMEM 172 192 POTENTIAL.
FT DOMAIN 193 223 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 224 244 POTENTIAL.
FT DOMAIN 253 283 PORE-FORMING (BY SIMILARITY).
FT TRANSMEM 288 308 POTENTIAL.
FT DOMAIN 309 426 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 378 426 ESSENTIAL FOR CHLOROFORM AND HALOTHANE
SENSITIVITY (BY SIMILARITY).
FT DOMAIN 354 426 REQUIRED FOR BASAL CHANNEL ACTIVITY (BY
SIMILARITY).
FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 2 16 MISSING (IN REF. 2).
FT CONFLICT 309 311 RLV -> DWL (IN REF. 2).
FT CONFLICT 391 391 S -> N (IN REF. 2).
FT CONFLICT 411 411 A -> T (IN REF. 2).
SQ SEQUENCE 426 AA; 47016 MW; 2ABR2336D4009F4E CRC64;

```

Query Match 98.2%; Score 2062; DB 1; Length 426;  
 Best local Similarity 98.5%; Pred. No. 1,le-130;  
 Matches 405; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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QY 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINVMKKTVSTFLVVLII 60
DB 16 VAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINVMKKTVSTFLVVLII 75
QY 61 GATVFKALDQPHETISORTTIVIOKOTFISQHSQVNSTEDELQOIVAAINAGIIPLGNT 120
DB 76 GATVFKALDQPHETISORTTIVIOKOTFISQHSQVNSTEDELQOIVAAINAGIIPLGNT 135
QY 121 SNOISIMDLSSFFAGTGTITGFGNISPRTGKIFCIITVALLGIPLEGFLAGVGDQ 180
DB 136 SNOISIMDLSSFFAGTGTITGFGNISPRTGKIFCIITVALLGIPLEGFLAGVGDQ 195
QY 181 LGTIFGKGLAKVEDTPIKMNVSQTKIRIISTIFILEGCVLFAVAPAIIFKHEIGMSALD 240
DB 196 LGTIFGKGLAKVEDTPIKMNVSQTKIRIISTIFILEGCVLFAVAPAIIFKHEIGMSALD 255
QY 241 AITFYVITTTTIGFGYVAGSGDIEYLDPKPYVWFWIIVGLAFPAVASMIGDMLRVIS 300
DB 256 AITFYVITTTTIGFGYVAGSGDIEYLDPKPYVWFWIIVGLAFPAVASMIGDMLRVIS 315
QY 301 KKTKEVGEFRAHAEMTANVTAEFKETRRRLSEVETDKFORATSIKRLKSLAELAGNHQ 360
DB 316 KKTKEVGEFRAHAEMTANVTAEFKETRRRLSEVETDKFORATSIKRLKSLAELAGNHQ 375
QY 361 ELTPCRRRLTSVNHLENERDYLPLPLKTESIYLLGLTPHCAGEIIVAVENIK 411
DB 376 ELTPCRRRLTSVNHLENERDYLPLPLKTESIYLLGLTPHCAGEIIVAVENIK 426
RESULT 2
CIN2_MOUSE STANDARD; PRT; 411 AA.
ID CIN2_MOUSE
AC P97438;
DR 01-OCT-2000 (rel. 40; Created)
DT 01-OCT-2000 (rel. 40; Last sequence update)
DE 01-OCT-2000 (rel. 40; Last annotation update)
DE POTASSIUM CHANNEL SUBFAMILY K MEMBER 2 (OUTWARD RECTIFYING POTASSIUM
CHANNEL PROTEIN TREK-1) (TWO-PORE POTASSIUM CHANNEL TPCK1) (TREK-1 K+
CHANNEL SUBUNIT).
GN KCNK2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
RC TISSUE=Brain;
RA MEDLINE=97157476; PubMed=9003761;
RA Fink M., Duprat F., Lesage F., Reyes R., Romey G., Heurteaux C.,
RA Lazdunski M.;

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RT "Cloning, functional expression and brain localization of a novel
RT unconv. conditional outward rectifier K+ channel.
RL EMBO J. 15:6854-6862(1996).
RN [2]
RP REVISIONS.
RC TISSUE=Brain;
RA Fink M., Duprat F., Lesage F., Reyes R., Romey G., Heurteaux C.,
RA Lazdunski M.;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RP ACTIVATION
RX MEDLINE=99254548; PubMed=10321245;
RA Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.;
RT "Inhalational anesthetics activate two-pore K+ channels in background K+
RT channels."
RL Nat. Neurosci. 2:422-426(1999).
CC -1- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL.
CC -1- SUBUNIT: HOMODIMER (POTENTIAL).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- TISSUE SPECIFICITY: HIGH EXPRESSION IN BRAIN AND LUNG. ALSO
CC DETECTED IN KIDNEY, HEART AND SKELETAL MUSCLE. NOT DETECTED IN
CC LIVER. IN THE BRAIN, HIGHEST EXPRESSION IN PREFRONTAL BULB,
CC HIPPOCAMPUS AND CEREBELLUM.
CC -1- MISCELLANEOUS: INHIBITED BY BARIUM. ACTIVATED BY VOLATILE GENERAL
CC ANAESTHETICS SUCH AS CHLOROFORM, DIETHYL ETHER, HALOTHANE AND
CC ISOFLURANE.
CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
CC CHANNELS.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC DR EMBL: U73488; AAC53005.2; -.
CC DR MGD: MGI:109366; Kcnk2.
CC DR InterPro: IPR000099; -.
CC DR InterPro: IPR001622; -.
CC DR InterPro: IPR003280; -.
CC DR Pfam: PF02034; TWIK_channel; 1.
CC DR PRINTS: PR01333; 2PORECHANNEL.
CC KW Ionic channel; Transmembrane; Ion transport; Potassium transport;
CC Glycoprotein.
FT DOMAIN 1 46 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 47 67 POTENTIAL.
FT DOMAIN 129 155 PORE-FORMING (POTENTIAL).
FT TRANSMEM 157 177 POTENTIAL.
FT DOMAIN 178 207 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 208 228 POTENTIAL.
FT DOMAIN 238 268 PORE-FORMING (POTENTIAL).
FT TRANSMEM 273 293 POTENTIAL.
FT DOMAIN 294 411 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 378 411 ESSENTIAL FOR CHLOROFORM AND HALOTHANE
SENSITIVITY.
FT DOMAIN 354 411 REQUIRED FOR BASAL CHANNEL ACTIVITY.
FT CARBOHYD 95 95 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 411 AA; 45297 MW; 8F976DD103EFDV05 CRC64;

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Query Match 97.2%; Score 2041; DB 1; Length 411;  
 Best local Similarity 96.1%; Pred. No. 2,7e-129;  
 Matches 395; Conservative 12; Mismatches 4; Indels 0; Gaps 0;

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QY 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINVMKKTVSTFLVVLII 60
DB 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINVMKKTVSTFLVVLII 60
QY 61 GATVFKALDQPHETISORTTIVIOKOTFISQHSQVNSTEDELQOIVAAINAGIIPLGNT 120

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Db 61 GAAVFAKLEPOEISQRTTIVYIOKQFIQAHCACVNSTELDELIOQIYAALNAGIIPLGNS 120
QY 121 SNOISHMDLSSPEFFACTVITTTIGFNGISPRTEGKIFCIITIALGIPFLGAGVDQ 180
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 SNOISHMDLSSPEFFACTVITTTIGFNGISPRTEGKIFCIITIALGIPFLGAGVDQ 180
QY 181 LGTIFGKIAKVEDTFTKMNVSQTKIRIISTIFILFGCVLPAIIFKHIGMSALD 240
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 LGTIFGKIAKVEDTFTKMNVSQTKIRIISTIFILFGCVLPAIIFKHIGMSALD 240
QY 241 AIFEVVTLTTIGFQDVAGSDIEYDFKPYVMFVLVGLAFAVLSIGMLRVIS 300
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 AIFEVVTLTTIGFQDVAGSDIEYDFKPYVMFVLVGLAFAVLSIGMLRVIS 300
QY 301 KKTREEVEFRANAAEMTAVTAEFKTRRLRSVEIYDKFORATSIKRLSAELAGHNQ 360
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 KKTREEVEFRANAAEMTAVTAEFKTRRLRSVEIYDKFORATSIKRLSAELAGHNQ 360
QY 361 ELTPCRRTLISVNLITNERDVLPLPKTESIYLNGLPHCAGEEIAVENIK 411
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 361 ELTPCRRTLISVNLITNERDVLPLPKTESIYLNGLPHCAGEEIAVENIK 411

RESULT 3
C1M4_HUMAN STANDARD: PRT; 393 AA.
AC 09NYG8;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE POTASSIUM CHANNEL SUBFAMILY K MEMBER 4 (TWIK-RELATED ARACHIDONIC ACID-
  STIMULATED POTASSIUM CHANNEL PROTEIN) (TRAAK).
GN KCNK4 OR TRAAK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Brain;
RX PubMed=11042359;
RA Chapman C.G., Meadows H.J., Godden R.J., Campbell D.A., Duckworth M.,
  Kelsell R.E., Muddock P.R., Randall A.D., Rennie G.T., Gloger I.S.;
  "Cloning, localisation and functional expression of a novel human,
  RT cerebellum specific, two pore domain potassium channel.";
  RL Brain Res. Mol. Brain Res. 82:74-83(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Frontal cortex;
RA Gray A.T.;
RT "Assignment of KCNK4 encoding the human potassium channel TRAAK to
  RT chromosome 11.";
  RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: VOLTAGE INSENSITIVE, INSTANTANEOUS, OUTWARDLY RECTIFYING
  CC POTASSIUM CHANNEL. OUTWARD RECTIFICATION IS REVERSED AT HIGH
  CC EXTERNAL K+ CONCENTRATIONS (BY SIMILARITY).
  CC -1- SUBUNIT: HOMODIMER (POTENTIAL).
  CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
  CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
  CC CHANNELS.
  CC -----
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  CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
  CC or send an email to license@sib-sib.ch).
  CC -----
  CC EMBL: AF248242; AAC31731.1;
  CC EMBL: AF247042; AA64062.1; ALT_INIT.
  CC DR EMBL: AF247042; AA64062.1; ALT_INIT.
  CC DR InterPro: IPR001622;
  CC DR InterPro: IPR003280;

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DR PRINTS; PRO1333; 2PORECHANNEL.
KW Ionic channel; Transmembrane; Ion transport; potassium transport;
KM Glycoprotein.
FT DOMAIN 1 3
FT TRANSMEM 4 24
FT DOMAIN 89 113
FT TRANSMEM 118 138
FT DOMAIN 140 171
FT TRANSMEM 172 192
FT DOMAIN 197 221
FT TRANSMEM 234 254
FT DOMAIN 255 393
FT CARBOHYD 78 78
FT CARBOHYD 82 82
FT CONFLICT 328 328
FT CONFLICT 42704 MW; 7E1B53A0A9A
SQ SEQUENCE 393 AA; 42704 MW; 7E1B53A0A9A

Query Match 38.28; Score 803; DB Length 393;
Best Local Similarity 51.14; Pred. No. 8.6e
Matches 145; Conservative 61; Mismatches

QY 42 MKKTVSTIFLYVAVYLLIGATVFKALEPHEISQRTT KQFIQSHSCVNSTELDE 101
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MRSTLLALLLVLLVLSGALVFALEQPHQQAQREI KFLNAPCVSDQELGL 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 102 LIQOIVAINAGIIPLGNTSNOISH--WDLSSPEFFAG GFCNISPRTEGKIFC 159
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 LIKEVAALGGGAPERNSTSSSHSAMDLSAFAFFSG GYGVALRTAGRLFC 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 160 IIVALLGIPLEFLLAGVGDLGTFIFGKIAKVEDTFTK KTKRIISTIFILFGC 219
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 IFYALVGIPLEFLLAGVGDLGSSLRHIGIHIAIFLKL PLVAVLSAMFLFLIGC 180
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 220 VLFAALRAIFKHIEGMSALDAIFVYITLTTFEGD KIEVLDPFKPYVMFVL 279
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 LFLVLPTEFVCEMEDSKLEAIFVITVTTTGVGVVA KPROSPAVQPLWFWIL 240
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 280 VGLAVFAVLSMIGDMLRVISKKTREEVEFRANAA KKTREEVEFRANAA 323
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 LGLAVFASVLTITIGNMLRVYSKRTAREMGILTAQASH KKTREEVEFRANAA 284
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 4
C1M4_MOUSE STANDARD: PRT; 398 AA.
AC 068454;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE POTASSIUM CHANNEL SUBFAMILY K MEMBER 4 (TWIK-
  STIMULATED POTASSIUM CHANNEL PROTEIN) (TRAAK).
GN KCNK4 OR TRAAK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Brain;
RX MEDLINE=98292450; PubMed=9628867;
RA Pink M., Lesage F., Duprat F., Heurteaux C., Flocke S.R., Fosset M.,
  Lazdunski M.;
  RT "A neuronal two p domain K+ channel stimulates arachidonic acid and
  RT polyunsaturated fatty acids.";
  RL EMBO J. 17:3297-3308(1998).
RN [2]
RP ACTIVATION.
RX MEDLINE=99254548; PubMed=10321245;
RA Patel A.J., Honore E., Lesage F., Pink M., Lazdunski M.;
  RT "Inhalational anesthetics activate two-pore-domain background K+
  RT channels.";
  RL Nat. Neurosci. 2:422-426(1999).

```

CC -1- FUNCTION: VOLTAGE INSENSITIVE, INSTANTANEOUS, OUTWARDLY RECTIFYING  
 CC POTASSIUM CHANNEL. OUTWARD RECTIFICATION IS REVERSED AT HIGH  
 CC EXTERNAL K+ CONCENTRATIONS.  
 CC -1- SUBUNIT: HOMODIMER (POTENTIAL).  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND  
 CC 2/TRANSP/TRANSCATED; ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, SPINAL CORD AND EYE. NOT  
 CC DETECTED IN HEART, SKELETAL MUSCLE, LIVER, LUNGS, KIDNEY AND  
 CC TESTIS.  
 CC -1- MISCELLANEOUS: ACTIVATED BY ARCHIDONIC ACID AND OTHER UNSATURATED  
 CC FATTY ACIDS. NOT AFFECTED BY VOLATILE GENERAL ANESTHETICS SUCH AS  
 CC CHLOROFORM, DIETHYL ETHER, HALOTHANE AND ISOFLURANE.  
 CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM  
 CC CHANNELS.  
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 CC -----  
 CC EMBL: AF056492; AAC40181.1; -  
 CC DR MGD: MGI:1298234; Kcnk4.  
 CC DR InterPro: IPR000099; -  
 CC DR InterPro: IPR001622; -  
 CC DR InterPro: IPR003280; -  
 CC DR Pfam: PF02034; TWIK\_channel.1.  
 CC DR PRINTS: PR01333; 2PORECHANNEL.  
 CC DR KMW: KMW:K1333; 2PORECHANNEL.  
 CC KW Glycoprotein; Alternative splicing.  
 CC FT DOMAIN 1 3 CYTOPLASMIC (POTENTIAL).  
 CC FT TRANSMEM 4 24 POTENTIAL.  
 CC FT DOMAIN 89 113 PORE-FORMING (POTENTIAL).  
 CC FT TRANSMEM 119 139 POTENTIAL.  
 CC FT DOMAIN 140 192 CYTOPLASMIC (POTENTIAL).  
 CC FT TRANSMEM 172 192 POTENTIAL.  
 CC FT DOMAIN 198 232 PORE-FORMING (POTENTIAL).  
 CC FT TRANSMEM 235 255 POTENTIAL.  
 CC FT DOMAIN 256 398 CYTOPLASMIC (POTENTIAL).  
 CC FT CARBOHYD 81 84 N-LINKED (GLCNC. . .) (POTENTIAL).  
 CC FT CARBOHYD 84 84 N-LINKED (GLCNC. . .) (POTENTIAL).  
 CC FT VARSPPLIC 63 67 KILIVE -> KAMAI (IN ISOFORM 2).  
 CC FT VARSPPLIC 68 398 MISSING (IN ISOFORM 2).  
 CC SQ SEQUENCE 398 AA; 43051 MW; 478A834B7B7AEC92 CRC64;

Query Match 37.0%; Score 776.5; DB 1; Length 398;  
 Best Local Similarity 49.8%; Pred. No. 5.1e-45;  
 Matches 142; Conservative 57; Mismatches 83; Indels 3; Gaps 1;

QY 42 MKKRTVSTFLVYVYLLIGATYFKALQEPHEISORTTIVIOKOTFISQHCVNSTELDE 101  
 DB 1 MRSTTLALALALVLFVSGALFQALQEPHEISQAKKMDHGRDQLRHPHCKSOKSLED 60  
 QY 102 LIQOIYAAINAGTIP--LGNTSNOISHDHDSSEFFAGTITITFGNISPTEBGKIF 158  
 DB 61 FIKLIVLALGGANPEPTSMNTSSNANLGSAPFFSGITITITIGNVLHTDGRLE 120  
 QY 159 CIYVALGIPLEGFLAGVDDQGTIFGKIAKVEDFTIKMNSQTKRIITIFILFG 218  
 DB 121 CIFYVALVGPILGMLAGVDRGSLRGIGIEAIFLKNHPPLGLVSLAVFLLLG 180  
 QY 219 CUYVALPPIIRKHEGMSALDAIYFVITLTITGFDYVAGGSDIEYDEYKPVVWMI 278  
 DB 181 CLFVLTLPFVFSYMSKELAIYFVITLTITGFDYVAGGSDIYDEYKPVVWMI 240  
 QY 279 LVGLAFVAVLSIGMDLRFVISKTEEGEGRFAHAEMTANTTA 323  
 DB 241 LGLAFVAVLSITIGMDLRFVISKTEEGEGRFAHAEMTANTTA 285

RESULT 5  
 ID CITS\_HUMAN STANDARD: PRT; 499 AA  
 AC 095279;  
 DT 01-OCT-2000 (Rel. 40, Created)  
 DT 01-OCT-2000 (Rel. 40, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE POTASSIUM CHANNEL SUBFAMILY K MEMBER 5 (ACID-SENSITIVE POTASSIUM  
 DE CHANNEL PROTEIN TASK-2) (TWIK-RELATED ACID-SENSITIVE K+ CHANNEL 2).  
 GN KCNK3 OR TASK2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RX MEDLINE=99030343; PubMed=9812978;  
 RA Reyes R., Duprat F., Lesage F., Fink M., Saubermann A., Farnan N.,  
 RA Lazdunski M.,  
 RT Cloning and expression of a novel pH-sens. two pore domain K+  
 RT channel from human kidney.  
 RL J. Biol. Chem. 273:30863-30869(1998).  
 CC -1- FUNCTION: PH DEPENDENT, VOLTAGE INSENSITIVE, OUTWARDLY RECTIFYING  
 CC POTASSIUM CHANNEL. OUTWARD RECTIFICATION IS LOST AT HIGH EXTERNAL  
 CC K+ CONCENTRATIONS.  
 CC -1- SUBUNIT: HOMODIMER (POTENTIAL).  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).  
 CC -1- TISSUE SPECIFICITY: ABUNDANT EXPRESSION IN KIDNEY, ALSO DETECTED  
 CC IN LIVER, PLACENTA AND SMALL INTESTINE. IN THE KIDNEY, EXPRESSION  
 CC IS RESTRICTED TO THE DISTAL TUBULES AND COLLECTING DUCTS. NOT  
 CC EXPRESSED IN PROXIMAL TUBULES OR GLOMERULI.  
 CC -1- MISCELLANEOUS: INHIBITED BY QUININE, QUINIDINE AND EXTERNAL  
 CC ACIDIFICATION.  
 CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM  
 CC CHANNELS.  
 CC -----  
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 CC -----  
 CC EMBL: AF084830; AAC79458.1; -  
 CC DR MIM: 603493; -  
 CC DR InterPro: IPR000099; -  
 CC DR InterPro: IPR001622; -  
 CC DR InterPro: IPR003280; -  
 CC DR Pfam: PF02034; TWIK\_channel.1.  
 CC DR PRINTS: PR01333; 2PORECHANNEL.  
 CC KW Ionic channel; Transmembrane; Ion transport; Potassium transport;  
 CC Glycoprotein.  
 CC FT DOMAIN 1 7 CYTOPLASMIC (POTENTIAL).  
 CC FT TRANSMEM 8 26 POTENTIAL.  
 CC FT DOMAIN 85 112 PORE-FORMING (POTENTIAL).  
 CC FT TRANSMEM 113 133 POTENTIAL.  
 CC FT DOMAIN 134 157 CYTOPLASMIC (POTENTIAL).  
 CC FT TRANSMEM 158 180 POTENTIAL.  
 CC FT DOMAIN 190 215 PORE-FORMING (POTENTIAL).  
 CC FT TRANSMEM 230 250 POTENTIAL.  
 CC FT DOMAIN 251 325 CYTOPLASMIC (POTENTIAL).  
 CC FT CARBOHYD 77 77 N-LINKED (GLCNC. . .) (POTENTIAL).  
 CC SQ SEQUENCE 499 AA; 55130 MW; E871A7A4823D70B CRC64;

Query Match 20.3%; Score 427; DB 1; Length 499;  
 Best Local Similarity 31.1%; Pred. No. 1.3e-21;  
 Matches 106; Conservative 60; Mismatches 121; Indels 54; Gaps 11;

QY 54 VVYLIGATYFKALQEPHEISORTTIVIOKOTFISQHCVNSTELDELIQOIYAAINAG 113

```

Db 12 IIFLAIAGAAIFVELEPHKEAKNNYTKLHLKFEPCGQGLKILEVSDAAGG 71
Qy 114 IIPKLSNOISHDGSSFFACTVITTTGFCNISPRTGKIFCIYALGIPLEGFL 173
Db 72 VAINGNT--FNNMNMWNAIFATVITTTIGYGNVAKRTPAGRCFCYFGVGLP---C 126
Qy 174 LAGVGDLGTFPGKIAKVEDTFIKMVSQTKIRIISTITIFLFGCVLPAIPAIKRI 233
Db 127 LMTI-SALGFEFGGRKRLGCLFKRGVSLRKAQITCTVFIFVGVLVHIVPPEFVNT 185
Qy 234 EGMSALDAIFVVTITTTIGDGVAG--GSDIEYLDYKRPVWVWILVGLAYFAVLSMI 292
Db 186 EGMVYIGLYSFTTISTIGDGVAGVNSANHALRYFVELMTYGLAW---LSLF 241
Qy 293 GDMVLRVSKTKKEVGEFRAHAEMTAVTAEFKTRRLSVEIYDKFRATSIKRLISA 352
Db 242 VNM-----KVSME-----VEVKAIRKRRR-----RKESF 267
Qy 353 ELAGNHOELPCRRRLSVNHLNERDV--LPPLKTESIT 391
Db 268 E-SSPHS-----RKALQVKGSTASKDVNIFSFLSKKEEY 301

RESULT 6
CITL_HUMAN STANDARD; PRT; 336 AA.
AC 000180; Q13307;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DE POTASSIUM CHANNEL SUBFAMILY K MEMBER 1 (INWARD RECTIFYING POTASSIUM
DE CHANNEL PROTEIN TWIK-1) (POTASSIUM CHANNEL KCNO1).
GN KCNK1 OR TWIK1 OR HOHOL OR KCNO1.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A., FUNCTION, AND MUTAGENESIS OF THR-161.
RC TISSUE=Kidney;
RX MEDLINE=96183184; PubMed=8605869;
RA Lesage F., Guillemare E., Fink M., Duprat F., Lazdunski M., Romey G.,
RA Barhanin J.;
RT "TWIK-1, a ubiquitous human weakly inward rectifying K+ channel with a
RT novel structure.";
RL EMBO J. 15:1004-1011(1996).
[2]
RN SEQUENCE FROM N.A., AND REVIEW.
RC TISSUE=Brain;
RX MEDLINE=98122696; PubMed=9462864;
RA Goldstein S.A.N., Wang K.-W., Iian N., Pausch M.H.;
RT "Sequence and function of the two P domain potassium channels:
RT Implications of an emerging superfamily.";
RL J. Mol. Med. 76:13-20(1998).
[3]
RN SEQUENCE FROM N.A.
RP Desir G.V., Orlas M., Freeman T.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: WEAKLY INWARD RECTIFYING POTASSIUM CHANNEL.
CC -1- SUBUNIT: HOMODIMER (POTENTIAL).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGH LEVELS IN HEART AND
CC BRAIN AND LOWER LEVELS IN PLACENTA, LUNG, LIVER AND KIDNEY.
CC -1- MISCELLANEOUS: INHIBITED BY BARTOLIN, QUININE, QUINIDINE AND
CC INTERNAL ACIDIFICATION. ACTIVATED BY PROTEIN KINASE C.
CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
CC CHANNELS.
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CC -----
DR EMBL: U33632; AAB01688.1; -
DR EMBL: U76966; AAB97878.1; -
DR EMBL: U90065; AAB51147.1; -
DR MIM: 601745; -
DR InterPro: IPR000099; -
DR InterPro: IPR001622; -
DR InterPro: IPR001779; -
DR InterPro: IPR003280; -
DR Pfam: PF02034; TWIK_channel; 1.
DR PRINTS: PR01096; TWIK1CHANNEL.
DR PRINTS: PR01333; 2PORECHANNEL.
KW Ionic channel; Transmembrane; Ion transport; Potassium transport;
KW Glycoprotein.
FT DOMAIN 1 20 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 21 41 POTENTIAL.
FT DOMAIN 104 130 PORE-FORMING (POTENTIAL).
FT TRANSMEM 133 153 POTENTIAL.
FT DOMAIN 154 177 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 178 198 POTENTIAL.
FT DOMAIN 212 238 PORE-FORMING (POTENTIAL).
FT TRANSMEM 247 267 POTENTIAL.
FT DOMAIN 268 336 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 95 95 N-LINKED (GLYCOPOLYMER) (POTENTIAL).
FT MUTAGEN 161 161 T->A: NO EFFECT ON CHANNEL ACTIVITY.
SQ SEQUENCE 336 AA; 38143 MW; 2A41D9501323215D CRC64;

Query Match 18.1%; Score 379.5; Length 336;
Best Local Similarity 32.5%; Pred. No. 1.2e-16;
Matches 90; Conservative 62; Mismatches 11; Indels 17; Gaps 9;

Qy 51 FLVV-VLYLTGATVERKALEQPHISORTIVIOKTHISQSCWSTELDELIOQIVA 108
Db 25 FLVGLYLYLVGAVVSVSELPYEDLROELARKLRKRFLEHISCLSQQLDEPFLGRLE 84
Qy 109 AINNGIIPLGNTSQISHDGSSFFACTVITTTIGFCNISPRTGKIFCIYALGIP 168
Db 85 ASNIGVSVLSASGN-NWMDTSLAFRASTVSLSTTGTHVYVSDGGAFCITVSGTIP 143
Qy 169 LFGFLAGVGDLGTFPGKIAKVEDTFIKMVSQTKIRIISTITIFLFGCVLPAIP 226
Db 144 FTLLFLAVVGRIVVHTR--RPVLFIRIKRGFSKQVAVIAHVLGVTVSCFFI--P 199
Qy 227 AIFRKHI-EGMSALDAIFVVTITTTIGDGVAG--GSLIYLDYKRPVWVWILVGLAY 284
Db 200 AAVSFLEDDWNLFESEFYCFISLTIGLDYVGEGVNCKFRFLRYIGTICVLLGLIA 259
Qy 285 FAVLSMIGMLRYISK-----KTKKEVGEFRAHA 316
Db 260 MLVYLETFCE-LHBLKFRKMFYVKKDKDEDAVHIE 295

RESULT 7
CITL_MOUSE STANDARD; PRT; 336 AA.
AC 008581;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DE POTASSIUM CHANNEL SUBFAMILY K MEMBER 1 (INWARD RECTIFYING POTASSIUM
DE CHANNEL PROTEIN TWIK-1).
GN KCNK1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathii; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN RP SEQUENCE FROM N.A.
RC TISSUE=Brain;

```

RX MEDLINE=97165959; PubMed=9013852;  
 RA Lesage F., Lauritzen I., Duprat F., Reyes R., Fink M., Heurteaux C.,  
 RA Lazdunski M.;  
 RT "The structure, function and distribution of the mouse TWIK-1 K+  
 RT channel.";  
 RL FEBS Lett. 402:28-32(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/SVJ; TISSUE=Liver;  
 RX MEDLINE=98218573; PubMed=9559671;  
 RA Arrighi I., Lesage F., Scimeca J.-C., Carle G.F., Barhanin J.;  
 RT "Structure, chromosome localization, and tissue distribution of the  
 RT mouse twik K+ channel gene.";  
 RL FEBS Lett. 425:310-316(1998).  
 CC -1- FUNCTION: WEAK INWARDLY RECTIFYING POTASSIUM CHANNEL.  
 CC -1- SUBUNIT: HOMODIMER (POTENTIAL).  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).  
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED. HIGHEST EXPRESSION IN BRAIN,  
 CC KIDNEY, THYROID, SALIVARY GLAND, ADRENAL GLAND, PROSTATE,  
 CC EPIDIDYMIS, UTERUS, PLACENTA, COLON AND JEJUNUM. MODERATE  
 CC EXPRESSION IN EYES, PITUITARY, PANCREAS, SMOOTH MUSCLE, TESTIS AND  
 CC OVARY. VERY LOW LEVELS IN LUNG, AORTA, LIVER, HEART, SKELETAL  
 CC MUSCLE, THYMUS AND SPLEEN. IN THE BRAIN, HIGHEST EXPRESSION IN  
 CC CEREBELLAR GRANULE CELLS, BRAINSTEM, HIPPOCAMPUS AND CEREBRAL  
 CC CORTEX.  
 CC -1- DEVELOPMENTAL STAGE: EXPRESSION DETECTED AS EARLY AS 7 DAYS POST  
 CC CONCEPTION. EXPRESSION INCREASES FROM 2-8 DAYS AFTER BIRTH AND  
 CC STABILIZES AFTER DAY 8.  
 CC -1- MISCELLANEOUS: INHIBITED BY QUININE, BARIUM, AND INTERNAL  
 CC ACIDIFICATION. ACTIVATED BY PROTEIN KINASE C.  
 CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM  
 CC CHANNELS.  
 CC -----  
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 CC -----  
 DR EMBL: AF033017; AAC16973.1; -;  
 DR MGD; MG1:109322; KconK1.  
 DR InterPro: IPR000099; -;  
 DR InterPro: IPR001622; -;  
 DR InterPro: IPR001779; -;  
 DR InterPro: IPR003280; -;  
 DR Pfam: PF02034; TWIK\_channel.1.  
 DR PRINTS: PRO1096; TWIK1CHANNEL.  
 DR PRINTS: PRO1333; 2PORECHANNEL.  
 DR Ionic channel; Transmembrane; Ion transport; Potassium transport;  
 KW Glycoprotein.  
 FT DOMAIN 1 20 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 21 41 POTENTIAL.  
 FT DOMAIN 104 130 PORE-FORMING (POTENTIAL).  
 FT TRANSMEM 133 153 POTENTIAL.  
 FT DOMAIN 154 177 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 178 198 POTENTIAL.  
 FT DOMAIN 212 238 PORE-FORMING (POTENTIAL).  
 FT TRANSMEM 247 267 POTENTIAL.  
 FT DOMAIN 268 336 CYTOPLASMIC (POTENTIAL).  
 FT CAROHYD 95 95 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SO SEQUENCE 336 AA; 38275 MW; A996060A18266FD4 CRC64;

Query Match 17.6%; Score 370.5; DB 1; Length 336;  
 Best Local Similarity 33.9%; Pred. No. 4.9e-18;  
 Matches 83; Conservative 57; Mismatches 94; Indels 11; Gaps 7;

QY 51 FLVW--VLTLLIGATYFKLEQPHSEISORTTIVYKOTFISQSCNSVDELDELIOIYA 108  
 DB 25 FLVGLLTLYLVGAVVSESLPEYEDLLKROELKRLRFLLEHECLSEPOLDFLGRLVE 84

QY 109 AINAGIIPLGNTSNOISHMDLGSFFFACTVITIGFNG FEGGKIFCIYALLGIP 168  
 DB 85 ASNYGVSYSNMSGN-WMNDFTSALEFFASTVLSITGVC LBDGKAFCIIISYIGIP 143  
 QY 169 LFGFLLAGVGDOLGTIEGKIARKEDEDTFKMVSQTKI TII--FTLFGCVLFPALP 226  
 DB 144 FTLFLFTALVORTVAVTR--RPVLYFHIRMGFSKOVNA FAVLLGFTVSCFFPI--P 199  
 QY 227 AIIFFKIE-GMSALDIYVVTITITIGRDYVAG-GS LDPFKPVWMIWGLAY 284  
 DB 200 AANFVSLEDMDNPLESFYCFSLSTIGLADYVPGEGYV RELYKIGITCYLLGLIT 259  
 QY 285 PAAVL 289  
 DB 260 MLVVL 264  
 RESULT 8  
 C1W3\_HUMAN STANDARD; PRT; 394 AA.  
 AC 014649;  
 DT 01-OCT-2000 (rel. 40; Created)  
 DT 01-OCT-2000 (rel. 40; Last sequence update)  
 DT 01-OCT-2000 (rel. 40; Last annotation update)  
 DE POTASSIUM CHANNEL SUBFAMILY K MEMBER 3 (ACIF. POSITIVE POTASSIUM  
 DE CHANNEL PROTEIN TASK) (TWIK-RELATED ACID-SENS. IVE K+ CHANNEL).  
 GN KCNK3 OR TASK.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 ON NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RX MEDLINE=97459932; PubMed=9312005;  
 RA Duprat F., Lesage F., Fink M., Reyes R., Heurteaux C., Lazdunski M.;  
 RT "TASK, a human background K+ channel to sense external pH variations  
 RT near physiological pH.";  
 RL EMBO J. 16:5464-5471(1997).  
 RN [2]  
 RP ACTIVATION  
 RX MEDLINE=99254548; PubMed=10321245;  
 RA Patel A.J., Honore E., Lesage F., Fink M., Rom. G., Lazdunski M.;  
 RT "Inhalational anesthetics activate two-pore-domain background K+  
 RT channels.";  
 RL Nat. Neurosci. 2:422-426(1999).  
 CC -1- FUNCTION: PH-DEPENDENT, VOLTAGE-INSENSITIVE. BACKGROUND POTASSIUM  
 CC CHANNEL PROTEIN. RECTIFICATION DIRECTION: OUT. ION CURRENT FROM POTASSIUM  
 CC ION CONCENTRATION ON EITHER SIDE OF THE MEMBRANE. ACTS AS AN  
 CC OUTWARD RECTIFIER WHEN EXTERNAL POTASSIUM CONCENTRATION IS LOW.  
 CC WHEN EXTERNAL POTASSIUM CONCENTRATION IS HIGH, CURRENT IS INWARD.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).  
 CC -1- TISSUE SPECIFICITY: WIDESPREAD EXPRESSION IN ADULT. STRONGEST  
 CC EXPRESSION IN PANCREAS AND PLACENTA. LOW EXPRESSION IN BRAIN,  
 CC LUNG, PROSTATE, HEART, KIDNEY, UTERUS, AND INTESTINE AND COLON.  
 CC -1- MISCELLANEOUS: INHIBITED BY EXTERNAL ACIDIFICATION. ACTIVATED BY  
 CC HALOTHANE AND ISOFLURANE.  
 CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM  
 CC CHANNELS.  
 CC -----  
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 CC -----  
 DR EMBL: AF006823; AAC51777.1; -;  
 DR MIM: 603220; -;  
 DR InterPro: IPR000099; -;  
 DR InterPro: IPR001622; -;  
 DR InterPro: IPR003092; -;







(WHEN EXTERNAL POTASSIUM CONCENTRATION IS HIGH, CURRENT IS INWARD  
BY SIMILARITY).

-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).  
-1- TISSUE SPECIFICITY: STRONGEST EXPRESSION IN HEART. MODERATE  
EXPRESSION IN LUNG AND BRAIN. LOW LEVELS IN LIVER, KIDNEY AND  
SKELETAL MUSCLE.  
-1- MISCELLANEOUS: INHIBITED BY EXTRACELLULAR ACIDIFICATION, ZINC,  
BIPHYACATINE AND PHENYTOIN. ACTIVATED BY PROTEIN KINASE A.  
-1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM  
CHANNELS.

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CC CC -----

DR EMBL AF031384; AAC39952.1; -  
DR InterPro: IPR000099; -  
DR InterPro: IPR001622; -  
DR InterPro: IPR003092; -  
DR InterPro: IPR003280; -  
DR Pfam: PF02034; TWIK\_channel; 1.  
DR PRINTS: PR01095; TASKCHANNEL.  
DR PRINTS: PR01333; 2PORECHANNEL.  
KW Ionic channel; Transmembrane; Ion transport; Potassium transport;  
KM Glycoprotein.

FT DOMAIN 1 8 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 9 29 POTENTIAL.  
FT DOMAIN 78 101 PORE-FORMING (POTENTIAL).  
FT TRANSMEM 108 128 POTENTIAL.  
FT DOMAIN 129 158 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 159 179 POTENTIAL.  
FT DOMAIN 184 207 PORE-FORMING (POTENTIAL).  
FT TRANSMEM 223 243 POTENTIAL.  
FT DOMAIN 244 411 CYTOPLASMIC (POTENTIAL).  
FT CABOXYD 53 53 N-LINKED (GLCNAC... ) (POTENTIAL).  
SQ SEQUENCE 411 AA; 45276 MW; D2778016E09E2BF5 CRC64;

Query Match 16.3%; Score 343; DB 1; Length 411;  
Best Local Similarity 29.9%; Pred. No. 4.1e-16;  
Matches 88; Conservative 62; Mismatches 102; Indels 42; Gaps 9;

OY 42 MKMKVSTPIFLV--VLKLIIGATVPFKALQEPHEISORTTYIOKOTFISOHCVNS--T 97  
DB 1 MKRQWRTLLALVCCTFTLLTGAAVFADLSEPEIEIKORLEKOLELRARNLSSEGVE 60

OY 98 ELDELIIQIVAINAGIIRPLGNTSNQISHMDGSFFAGVTYITIGNISPTREGKI 157  
DB 61 ELEERVAVLR-KPKRGV-----QMRPGSFYTAITYITTIIGYCHAPSPDGKV 108

OY 158 FCIIVALLGIPLFGFLTAGVGDOGLCTIFGKGIAKYVEDFIKKNVSSQT-----IRI 208  
DB 109 FCMFYALLGIPLTLTMFOSLGRI-----NFEVRLLHRAXGLGMRAAEVSM 156

OY 209 ISTIIFILEGCVLPAALAIIFKHIEGMSALDAIFYVITLTITTFGGDVAGGSD--LEX 266  
DB 157 ANMVIIGFVSICSTLCIGAALAFSYIERMTFCFAVYYCCTTTTTTTTIFGDVALOKDQAL 216

OY 267 LDFFYPVMFWMLTVGLAFAVAVLSMGWLRYISKTKTEEVEGFSAHAAEWTAN 320  
DB 217 QPYVAEFSEVYIITGLTYIGAFLNLV--VLKRMTNMADEKRD-AEHRLALLTHN 267

RESULT 12  
ORNL\_DROME STANDARD: PROT: 1001 AA.  
AC 094526;  
DT 01-OCT-2000 (Rel. 40, Created)  
DT 01-OCT-2000 (Rel. 40, Last sequence update)

01-OCT-2000 (Rel.: 40, Last annotation update: 2000-10-01) PORE DOMAIN POTASSIUM CHANNEL ORK1.

Drosophila melanogaster (Fruit fly).

OS ORK1 OR CG1615.

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta; Diptera; Pterygota; Neoptera; Endopterygota; Chytrata; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

CC NCBI\_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Larva:

CC MEDLINE=91075152; PubMed=8917578;

RX Adams M.D., Celiker S.E., Holt R.A., Evans G.C., Gocayne J.D., Goldstein S.A.N., Price L.A., Rosenthal D.N., Schaefer A.L., Smith M.H.; "ORK1, a potassium-selective leak channel cloned from Drosophila melanogaster by expressed sequence analysis."

RT Proc. Natl. Acad. Sci. U.S.A. 93:13256-13261 (1996).

RL [2]

RN SEQUENCE FROM N.A.

RP STRAIN-BERKELEY;

RC MEDLINE=20196006; PubMed=10731132;

RX Gloder A., Gong F., Gorrell J.H., Gu Z., Gutierrez K., Harris N.L., Harvey D., Heiman T.J., Hernandez H., Hostin D., Houston K.A., Howland T.J., Mei J., Jaiswal M., Kalish F., Karpen G.H., Ke Z., Kimel B.E., Kodira C.D., Kraft C., Kravitz I., Laiko P., Lei Y., Levitsky A.A., Li J., Li Liu X., Mattei B., McIntosh T.C., McLeod M.I., Merkulov G., Mishina N.V., Mobarry C., Mori M., Mount S.M., Moy M., Murphy B., Murphy L., Nelson D.R., Nelson K.A., Nixon K., Nusskern J., Palazzolo M., Pittman G.S., Pan S., Pollard R., Reinert K., Remington K., Saunders R.D.C., Schneider F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skup M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Stutter E., Sun E., Svrtkas R., Tector C., Turner R., Venter J., Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J., Williams S.M., Woodage T., Wolley K.C., Wu L., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhao M., Zhou L., Zhong X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."

RT Science 287:2185-2195(2000).

RL -1- FUNCTION: BACKGROUND POTASSIUM CHANNEL. DIFFERENTIATION IS DEPENDENT ON EXTERNAL POTASSIUM CONCENTRATION. ACTS AS AN OUTWARDLY RECTIFYING CHANNEL BUT AS EXTERNAL POTASSIUM LEVELS INCREASE, THIS IS REVERSED.

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).

CC -1- TISSUE SPECIFICITY: WIDESPREAD EXPRESSION IN ADULT, STRONGEST EXPRESSION IN MUSCLE, BRAIN AND OVARY. ALSO PRESENT AT LOW LEVELS IN LARVA AND EMBRYO.

CC -1- MISCELLANEOUS: INHIBITED BY BARIUM.

CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM CHANNELS.

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RP SEQUENCE FROM N.A.  
RC STRAIN-BRISTOL N2;  
RX MEDLINE-94150718; PubMed-7906398;  
RA Wilson R., Almscough R., Anderson K., Baynes C., Berks M.,  
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,  
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,  
RA Fullon L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,  
RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,  
RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,  
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,  
RA Sims M., Smaiden N., Smith A., Smith M., Sonhammer E., Staden R.,  
RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,  
RA Waterston R., Watson A., Weinstein L., Wilkinson-Sproat J.,  
RA Wohldman P.;  
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
elegans.";  
RL Nature 368:32-38(1994).  
CC -i- SIMILARITY: TO POTASSIUM CHANNEL PROTEIN HAK-6.  
CC -----  
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DR WormBep: F22B7.7; CE00160.  
SQ SEQUENCE 335 AA; 38472 MW; 27DE7F1E79B3CA29 CRC64;  
  
Query Match 10.4%; Score 217.5; DB 1; Length 335;  
Best Local Similarity 26.7%; Pred. No. 7.7e-08;  
Matches 60; Conservative 37; Mismatches 75; Indels 53; Gaps 7;  
  
QY 120 TSNQISH-----WDLGSSFFRAGVYTTTIGFNGNISPRTEGKIFCIYALLGIPLEGL 173  
DB 15 TSNEVKKMATETWTFSSSIFFAVVTITGYGNPVPVNTIGRIMCILFSLGIPL--T 71  
QY 174 LAGVGDLGTIRGKIFAKYEDPFK-----NNVSQT 204  
DB 72 LVTIAD-LKFLSEHLVWLXGNTLKLKYLILSRHKKRERHVECHSHGMHNMIEEK 130  
QY 205 KIRIISFIIFLFGCVLFAVLPALIFKHIKIEGMSALDAIFYVVTITTTIGFGDYVAGGSDI 264  
DB 131 RI----PAFLVLAIIIVYTAFGVLSKLEPMSEFTSFYWSFITMTYVGGDLMPRRDGY 186  
QY 265 EYIDF-----YKPVVFWLIVGLAFPAVLSMIG--DWLRVI 299  
DB 187 MYILLIYIILGKFSMKKOKFKIFIGLAIYTMCIDLVGVQYIRKI 231

Search completed: August 28, 2001, 17:13:13  
Job time: 407 sec